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OM protein - protein search, using sw model

Run on: October 28, 2005, 17:47:28 ; Search time 43 Seconds
(without alignments)
484.351 Million cell updates/sec

Title: US-09-769-744D-26
Perfect score: 1387
Sequence: 1 MGIALENVNTYQEGTPLAS.....GVSPKRLPIKIEPKESLNG 279

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCUTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1386	99.9	279	4	US-09-583-110-4380
2	1386	99.9	280	4	US-09-107-433-4838
3	844.5	60.9	316	4	US-09-134-000C-4732
4	836.5	60.3	284	4	US-09-107-532A-6030
5	608	43.8	288	3	US-09-134-001C-3292
6	543	39.1	180	4	US-09-214-307A-2
7	508	36.6	300	4	US-09-861-451A-42
8	468.5	33.8	285	4	US-09-107-532A-6376
9	435.5	31.4	272	4	US-09-134-000C-4733
10	412.5	29.7	261	4	US-09-583-110-4382
11	402	29.0	290	3	US-09-134-001C-3273
12	396.5	28.6	249	4	US-09-107-433-4031
13	381.5	27.5	350	4	US-09-107-532A-6978
14	378.5	27.3	357	4	US-09-134-000C-4963
15	373	26.9	361	4	US-09-107-532A-6490
16	371	26.7	264	4	US-09-134-000C-6301
17	368	26.5	247	4	US-09-134-000C-4300
18	366.5	26.4	281	4	US-09-489-039A-10009
19	357	25.7	272	4	US-09-861-451A-4
20	356	25.7	247	4	US-09-107-532A-4327
21	354.5	25.6	353	4	US-09-583-110-4827
22	352	25.4	286	4	US-09-540-236-2931
23	351	25.3	265	4	US-09-710-279-2500
24	348	25.1	246	4	US-09-583-110-4713
25	348	25.1	255	4	US-09-107-433-3563
26	348	25.1	402	4	US-09-107-532A-5360
27	347.5	25.1	246	4	US-09-489-039A-13116

28	346	24.9	242	4	US-09-583-110-2985	Sequence 2985, Ap
29	346	24.9	245	4	US-09-107-433-4827	Sequence 4827, Ap
30	345.5	24.9	254	4	US-09-902-540-16627	Sequence 16627, A
31	345	24.9	242	3	US-09-134-001C-3832	Sequence 3832, Ap
32	344.5	24.8	227	4	US-09-634-238-289	Sequence 289, App
33	344	24.8	369	4	US-09-328-352-6905	Sequence 6905, Ap
34	343	24.7	244	4	US-09-583-110-2710	Sequence 2710, Ap
35	342	24.7	244	3	US-08-919-573-2	Sequence 2, Appl1
36	342	24.5	244	3	US-08-919-573-4	Sequence 4, Appl1
37	340.5	24.5	198	4	US-10-162-012-36	Sequence 36, Appl1
38	339	24.4	317	4	US-09-134-000C-5339	Sequence 5339, Ap
39	338.5	24.4	248	3	US-09-134-001C-3731	Sequence 3731, Ap
40	337	24.3	357	3	US-09-134-001C-4891	Sequence 4891, Ap
41	334.5	24.1	265	4	US-09-489-039A-12065	Sequence 12065, A
42	332.5	24.0	258	4	US-09-328-352-4625	Sequence 4625, Ap
43	331	23.9	252	4	US-09-583-110-5309	Sequence 5309, Ap
44	331	23.9	360	4	US-09-543-681A-6466	Sequence 6466, Ap
45	330	23.8	319	4	US-09-489-039A-8116	Sequence 8116, Ap

ALIGNMENTS

RESULT 1

US-09-583-110-4380
; Sequence 4380, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus.
; FILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4380
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4380

Query Match 99.9%; Score 1386; DB 4; Length 279;
Best Local Similarity 99.6%; Pred. No. 5e-143;
Matches 278; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGIALENVNTYQEGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTLIQLLGLLVP	60
DB	1	MGIALENVNTYQEGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTLIQLLGLLVP	60
QY	61	QGSVRVFDTLTSTSKNKQIRKQVGLVQFAENQIFETVLKDVAFQFQNGVSEED	120
DB	61	QGSVRVFDTLTSTSKNKQIRKQVGLVQFAENQIFETVLKDVAFQFQNGVSEED	120
QY	121	AVKTAREKALVGDIDSLFDRSPFELSGGQRRVAIAGILAMPEAILVLDPEAGLDPLG	180
DB	121	AVKTAREKALVGDIDSLFDRSPFELSGGQRRVAIAGILAMPEAILVLDPEAGLDPLG	180
QY	181	RKELMTLTKLHOSGMTIVLTHLMDVAYANQVYMEKGRVKGKPSDVFQDVVFME	240
DB	181	RKELMTLTKLHOSGMTIVLTHLMDVAYANQVYMEKGRVKGKPSDVFQDVVFME	240
QY	241	EVOLGVPKITAFCKRLADRGVSFKRLPIKIEEPKESLNG	279
DB	241	EVOLGVPKITAFCKRLADRGVSFKRLPIKIEEPKESLNG	279

RESULT 2

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Denek
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6030:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...284
SEQUENCE DESCRIPTION: SEQ ID NO: 6030:
US-09-107-532A-6030

Query Match 60.3%; Score 836.5; DB 4; Length 284;
Best Local Similarity 59.2%; Pred. No. 6.1e-83;
Matches 161; Conservative 50; Mismatches 60; Indels 1; Gaps 1;

QY 1 MGIALENVFTYQEGTPLASALSVDLSLTIEDGYSYALIGHTSGKSTLQLLNGLLVP 60
Db 12 MDIRPEQVDFTYQNTPEQRALEFDINMTIKENSYALVGHGTSKSTLQHLNALVKPT 71
QY 61 QGSVRVFDLTITSTSKNDIRQIRKQVGLVFOFAENQIFETVLKDVAFGPQNFVSEED 120
Db 72 SGTVHGIRDIQDPTDNKMLKPIRKVGVGFQPEAQLFEETVAKDIAGPKNFVSEEE 131
QY 121 AVKTAREKALVGDLSLFDSPFELSGGQMRRAIAGILAMEPAIILVLDDEPTAGLDPLG 180
Db 132 ALVLAKETLEQVGLDESILERSPFELSGGQMRRAIAGILAMEPAIILVLDDEPTAGLDPOG 191
QY 181 RKELMTLTKLH-QSGMTIVLVTHLMDVVAEYANQVYMEKRLVKGKPSDVFQDVFM 239
Db 192 RKEMEMFWRLHKEQOITIVLVTHLMDVVAEYANQVYMEKRLVKGKPSDVFQDVFM 251
QY 240 BEVOLGVPKITAFCKRLADR-GVSFKRLPIKIEP 271
Db 252 KEKQLGVPTATEPAEELMAGMNFATLPLTAE 283

RESULT 6
US-09-214-307A-2
Sequence 2, Application US/09214307A
Patent No. 6544516
GENERAL INFORMATION:
APPLICANT: NEUTEC PHARMA PLC
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF INFECTIONS OF GRAM POSITIVE
TITLE OF INVENTION: COCCI
FILE REFERENCE: PM 259204
CURRENT APPLICATION NUMBER: US/09/214,307A
CURRENT FILING DATE: 1999-01-04
PRIOR APPLICATION NUMBER: PCT/GB97/01830
PRIOR FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: GB9614274.0
PRIOR FILING DATE: 1996-07-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 180
TYPE: PRT
ORGANISM: Enterococcus faecium
US-09-214-307A-2

Query Match 39.1%; Score 543; DB 4; Length 180;
Best Local Similarity 62.4%; Pred. No. 3.6e-51;
Matches 106; Conservative 26; Mismatches 38; Indels 0; Gaps 0;

QY 7 NVNFTYQEGTPLASALSVDLSLTIEDGYSYALIGHTSGKSTLQLLNGLLVP 66
Db 11 NSRFTYQNTPEQRALEFDINMTIKENSYALVGHGTSKSTLQHLNALVKPTSGTVHI 70
QY 67 FDTLITSTSKNDIRQIRKQVGLVFOFAENQIFETVLKDVAFGPQNFVSEEDAVKTAR 126
Db 71 GERDIQDPTDNKMLKPIRKVGVGFQPEAQLFEETVAKDIAGPKNFVSEEDAVKTAR 130
QY 127 EKLALVGDLSLFDSPFELSGGQMRRAIAGILAMEPAIILVLDDEPTAGL 176
Db 131 ETLEQVGLDESILERSPFELSGGQMRRAIAGILAMEPAIILVLDDEPTAGL 180

RESULT 7
US-09-861-451A-42
Sequence 42, Application US/09861451A
Patent No. 6759516
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific & Industrial Research Orga
TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences

US-09-134-001C-3292
Sequence 3292, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3292
LENGTH: 288
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3292

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; FILE REFERENCE: FF34033/01
; CURRENT APPLICATION NUMBER: US/09/861,451A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PP7273
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Deduced protein
; OTHER INFORMATION: sequence from clone PAD913
US-09-861-451A-42

Query Match          36.6%; Score 508; DB 4; Length 300;
Best Local Similarity 37.5%; Pred. No. 5.5e-47;
Matches 111; Conservative 49; Mismatches 90; Indels 46; Gaps 4;

QY 1 MGIALENVFTYQEGTPLASAAALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLVPS 60
Db 1 MKIAKATIKVIYDQKLPSLAKALDKVTTEINQGEFIAIIGQTSGKTTFIQHNNALLPD 60
QY 61 QGSVR--VFDTLTSTSKND-----IRQIRKOVGLVFOFAENQIPEE 101
Db 61 QGEIYLYFD-----SKNQEKLVVQKPRFRKKLKFINEIRRRVGVVFOFAEYQLFEQ 114
QY 102 TVLKDVAFQPNQFVSEBDVKTAREKALVIGIDSLDFDRSPFELSGGQMRVAIAGILA 161
Db 115 TIEKDIIFGAVSMGTPKNEAKKIAAEIIEVLGDSFLQKSPFELSGGQKRVAIAGILA 174
QY 162 MEPAILVLDEPTAGLDIPGRKELMTLFLKHLQSGMTIVLVTHLMDDDVAEYANQVVMK 221
Db 175 MDPDIIFDEPTAGLDIPQGLKMLBILDVLTKKGTIIILATHDLDSVLEWTKRCIFFK 234
QY 222 RLKVGKPSDVFDVVEEVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESL 277
Db 235 RIYDGDYTSILANNKFL-----IENKMLPTNLLNFKRL 269

RESULT 8
US-09-107-532A-6376
; Sequence 6376, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Denese
; REGISTRATION NUMBER: 40,489
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; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6376:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...285
; SEQUENCE DESCRIPTION: SEQ ID NO: 6376:
US-09-107-532A-6376

Query Match          33.8%; Score 468.5; DB 4; Length 285;
Best Local Similarity 40.7%; Pred. No. 1e-42;
Matches 107; Conservative 53; Mismatches 88; Indels 15; Gaps 6;

QY 3 IALENVNFTYQEGTPLASAAALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLVPSQ 62
Db 11 IELEKINYQPPD--LRPALKDVFTIDKGEWIAIIGHNSGKSTLAKTINGLLLPSSG 68
QY 63 SVRVFDLTITSTSKNKDIQIRKOVGLVFOFAENQIPEETVLKDVAFQPNQFVSEB-- 120
Db 69 IVKVGNGIIL---DBENITWIRQVMGVFQNPQDFVGSSTVEDDVAFLGNQGIPEEML 124
QY 121 -AVKTAREKALVIGIDSLDFDRSPFELSGGQMRVAIAGILAMEPAILVLDEPTAGLD 179
Db 125 VRVKDALEKVRMA---EFASREPARLSGGQKQKRVAGVVALRPDIILDEATSM 180
QY 180 GRKELMTLFFKL--HQSGMTIVLVTHLMDDDVAEYANQVVMKGLVKGKPSDVFDV 238
Db 181 GREVISTIKIKESQLTVISITHDIDEAAN--ANRILVMRQGLVREGTPEKIFSA 239
QY 239 MEEVQLGVPKITAFCKRLADRGV 261
Db 240 LIDLGLDLPFPPEKLKALKERG 262

RESULT 9
US-09-134-000C-4733
; Sequence 4733, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4733
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4733

Query Match          31.4%; Score 435.5; DB 4; Length 272;
Best Local Similarity 39.3%; Pred. No. 3.9e-39;
Matches 96; Conservative 53; Mismatches 88; Indels 7; Gaps 4;

QY 19 ASAAALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLVPSQSVRVFDLTITSTSKNK 78
Db 12 ASPALKDVFSIQGEWVAIIGHNSGKSTLAKTINGILLPAAGTIKVGGKELNEA---- 67
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	Qy	79	D I R Q T R K Q V G L V F Q P A E N Q I F E E T V L K D V A R G P O N F G V S E E D A V K T A R E K L A L V G D E S L	138
	Db	68	N W M D I R R Y M G V F Q N P D N Q F V G S T V E D D A F G L E N Q I P R D E M V E R V H D A L E R V M L D - F	126
	Qy	139	P O R S F P E L S G G O M R B V A T A G I L A M E P A T L V L D E T A G I D L P G R K E L M T L P K L - H O S G M T	197
	Db	127	A K R E P A R L S G G Q R V A G V A U R P D I I I L D E A T S M L D P E G R A E V I A T T Q K I K E S N I T	186
	Qy	198	I V L V T H L M D D V A E Y A N Q V Y V M E K R L V K G G K P S D V F Q D V F M E E V Q L G V P K I T A F C K R L A	257
	Db	187	V I S I T H D I D E A N - A N R I L V M R Q O L T W E G T P E K I F S A G E A L V E M G L D L F P P E K L V A L K	245
	Qy	258	D R G V	261
	Db	246	E R G V	249

RESULT 10
 US-09-583-110-4382
 ; Sequence 4382, Application US/09583110
 ; Patent No. 6699703
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al.
 ; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
 ; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
 ; FILE REFERENCE: PATH00-07A
 ; CURRENT APPLICATION NUMBER: US/09/583,110
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/107,433
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/085,131
 ; PRIOR FILING DATE: 1998-05-12
 ; PRIOR APPLICATION NUMBER: US 60/051,553
 ; PRIOR FILING DATE: 1997-07-02
 ; NUMBER OF SEQ ID NOS: 5322
 ; SEQ ID NO 4382
 ; LENGTH: 261
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-09-583-110-4382

	Query Match	29.7%	Score 412.5;	DB 4;	Length 261;
	Best Local Similarity	38.8%;	Pred. No. 1.2e-36;		
	Matches 90; Conservative	57;	Mismatches 76;	Indels 9;	Gaps 5;
Qy	3 IALENVNFTYQEGTGLASAAALSDVSLTIEDGTSYALICHTGSGKSTIQLLNGLLVPSQG	62			
	:::::	:::::	:::::	:::::	:::::
Dd	5 IDVKNLFLRYKENQNYD--VKDITFHVKGEMLSIVGHNGSGKSTTVRLIDGLEAESG	62			
	:::::	:::::	:::::	:::::	:::::
Qy	63 SVRVDFDLITSTSKNKQIRTKQVGLVFQFAENQIFETVLKDVAFGPQNFVGSEDAV	122			
	:::::	:::::	:::::	:::::	:::::
Dd	63 EIVDGQRILT---EENVNNTIRIQGMVFQNPDPQFVGATVEDDVAFLENGOGLSROBMK	118			
	:::::	:::::	:::::	:::::	:::::
Qy	123 KTAREKIALVGIDSLDRSPFELSGGOMRRVATAGILAMEPAILILDEPTAGLDPLCRK	182			
	:::::	:::::	:::::	:::::	:::::
Dd	119 KRVEAALLVGNLID-FKKREPARLSGGQKQKVATAGVVAPAILILDDEATSMLDPEGR	177			
	:::::	:::::	:::::	:::::	:::::
Qy	183 ELMTLFKKLKHS-GWTVLVLTMLMDDVAEYANQVYVMKEKHLVKGKPSDV F	233			
	:::::	:::::	:::::	:::::	:::::
Dd	178 ELIGTVGIKRDYDMVTISITHDIEEVA-MDSRVLVMKKGBIESTSSPRELF	228			
	:::::	:::::	:::::	:::::	:::::

RESULT 11
US-09-134-001C-3273
; Sequence 3273, Application US/09134001C
; Patent No.: 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13

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, PRIOR APPLICATION NUMBER: US 60/064,964
, PRIOR FILING DATE: 1997-11-08
, PRIOR APPLICATION NUMBER: US 60/055,779
, PRIOR FILING DATE: 1997-08-14
, NUMBER OF SEQ ID NOS: 5674
, SEQ ID NO 3273
, LENGTH: 290
, TYPE: prt
, ORGANISM: staphylococcus epidermidis
US-09-134-001C-3273

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Query Match 29.0%; Score 402; DB 3; Length 290;
Best Local Similarity 39.4%; Pred. No. 2e-35;
Matches 97; Conservative 51; Mismatches 88; Indels

[illegible]

RESULT 12

US-09-107-433-4031
; Sequence 4031, Application US/09107433
; Patent No. 6800744

NO. 0000741
 SERIAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
 SEQUENCES RELATING TO STREPT
 THERAPEUTICS

NUMBER OF SEQUENCES: 5206

NUMBER OF SEQUENCES: 3200
CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

CITY: WASHINGTON
STATE: Massachusetts

STATE: MASSACHUSETTS
COUNTRY: USA

COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:

COMPUTER READABLE FORM.
MEDIUM TYPE: CD-ROM ISO9660

MEDIUM TYPE: CD-ROM 1003000
COMPUTER: <Unknown>

COMPUTER: <UNKNOWN>
OPERATING SYSTEM: <Unknown>

OPERATING SYSTEM: <UNKNOWN>
SOFTWARE: <Unknown>

SOFTWARE: COMPTON
CURRENT APPLICATION DATA:

CURRENT AFFILIATION DATA:
APPLICATION NUMBER: US/09/107,433

AFFIDAVIT NUMBER: 00/05/10/100
 FILING DATE: 30-Jun-1998

FILING DATE: 30-Jun-1990
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131

AFFIDAVIT NUMBER: 007 003134
FILING DATE: May 12, 1998

FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553

AFFIDAVIT NUMBER: 00/051553
 FILING DATE: July 2, 1997

FILING DATE: JULY 2, 1997

ATTORNEY/AGENT INFORMATION:

ATTORNEI/AGENTI INFORMATION:
NAME: Ariniello, Pamela Deneke

NAME: ALLIERIO, Pamela Denise
REGISTRATION NUMBER: 40.489

REGISTRATION NUMBER: 10/103
REFERENCE/DOCKET NUMBER: GTC-011

REFERENCE/DOCKET NUMBER: GIC 011

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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TELEPHONE: (781) 693-3007
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TELEFAX: (701) 893-6277

```
; INFORMATION FOR SEQ ID NO: 4031:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 249 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;     ORGANISM: Streptococcus pneumoniae
;   FEATURE:
;     NAME/KEY: misc feature
;     LOCATION: (B) LOCATION 1...249
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4031:
US-09-107-433-4031

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Best Local Similarity 37.1%; Pred. No. 6.3e-35;
Matches 86; Conservative 59; Mismatches 78; Indels 9; Gaps 5;

QY 3 IALENNVTYQEGTPLASAAALSDVSLTIEDGSGKSTILQLLGLLVPSSQ 62
DB 11 IDVKNLSFRYKQNYD--VKDITFHVKRGEWLSIVGHGSGKSTTVRLIDGLLEASG 68
QY 63 SVRVFDTLITSTSKNKDIRKQVGLVFPQFAENQIPEETVLKDVAFQPGVGVSEDAV 122
DB 69 EIVDQGRLETL-----BENWNIRKQIGMVFQPDNFGVATVEDDVAFLGNQGLSRQENK 124
QY 123 KTAREKALVGDIDSLFDRSPFELSGGQMRVVAIAGILAMEPAIILVLDDEPTAGLDPLGRK 182
DB 125 KRVEALALVGLD--FKKREPARLSGGQKQKQVAGVVALRPAIILDEATSMIDPEGR 183
QY 183 ELMTLFLFKLHQS-GMTIVLVTHLMDDDVAEYANQVVMKGRVLKGGKPSDVF 233
DB 184 ELIGTVKGIKDYDMTVISITHDLSEIA-MSDRLLVLRKREISTSPREL 234

RESULT 13
US-09-107-532A-6978
; Sequence 6978, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Denene
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6978:
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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 350 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;     ORGANISM: Enterococcus faecium
;   FEATURE:
;     NAME/KEY: misc feature
;     LOCATION: (B) LOCATION 1...350
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6978:
US-09-107-532A-6978

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Best Local Similarity 40.7%; Pred. No. 4.7e-33;
Matches 96; Conservative 48; Mismatches 81; Indels 11; Gaps 6;

QY 3 IALENNVTYQEGTPLASAAALSDVSLTIEDGSGKSTILQLLGLLVPSSQ 62
DB 10 IQLTNVKKTF-NGKNGNIQAVNDVSLNVEKGDYIGVYGAGKSTLVRLNLGLLELPTSG 68
QY 63 SVRVFDTLITSTSKNKDIRKQVGLVFPQFAENQIPEETVLKDVAFQPGVGVSEDAV 122
DB 69 EIVNDQDITKL-KNKSLRTRFKKIGMIFQHF-NLLWSRTVLENIQLPLELAGVPKSKRK 126
QY 123 KTAREKALVGDIDSLFDRSPFELSGGQMRVVAIAGILAMEPAIILVLDDEPTAGLDPLGRK 182
DB 127 ERABELLRLVGL-SGRGQAVPSQLSGGQKQKQVAGIARALANDPEILLCCDEATSLDPTTE 185
QY 183 ELMTLFLFKLHQS-GMTIVLVTHLMDDDVAEYANQVVMKGRVLKGGKPSDVF 234
DB 186 EVDLLLAINKKLN--LTIVLITHEMNVRKCNKVAVMELGVKVEGDLTVFR 238

RESULT 14
US-09-134-000C-4963
; Sequence 4963, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4963
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4963

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Best Local Similarity 39.2%; Pred. No. 1e-32;
Matches 91; Conservative 52; Mismatches 84; Indels 5; Gaps 5;

QY 3 IALENNVTYQEGTPLASAAALSDVSLTIEDGSGKSTILQLLGLLVPSSQ 62
DB 3 IELKNISVTFQO-KKQETQAVQDVSLTIDKGDYIGVYGAGKSTLVRLNLGLLQRTAG 61
QY 63 SVRVFDTLITSTSKNKDIRKQVGLVFPQFAENQIPEETVLKDVAFQPGVGVSEDAV 122
DB 62 TVIINKENILTFSK-KELRQQRKKIGMIFQHF-NLMKERTIFSNDLKYSLGSKSERR 119
QY 123 KTAREKALVGDIDSLFDRSPFELSGGQMRVVAIAGILAMEPAIILVLDDEPTAGLDPLGRK 182
DB 120 QKISHLLELVGLSEKR-DAYPSQLSGGQKQKQVAGIARALANDPEILLCCDEATSLDPTTG 178
QY 183 ELMTLFLFKLHQS-GMTIVLVTHLMDDDVAEYANQVVMKGRVLKGGKPSDVF 233
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Mon Oct 31 10:58:12 2005

Db 201 ITHNQVVKVKEICNKNVAVNMEDGRIVEKSSIQIFSN 235

Search completed: October 28, 2005, 18:02:54
Job time : 44 secs

Db 179 QIILALKKLNQELNLTIVLITHMQVVKVKEICNKNVAVMENGCVVESNDIVSIF 230

RESULT 15
US-09-107-532A-6490
; Sequence 6490, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bueh
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6490:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...361
; SEQUENCE DESCRIPTION: SEQ ID NO: 6490:
US-09-107-532A-6490

Query Match 26.9%; Score 373; DB 4; Length 361;
Best Local Similarity 40.5%; Pred. No. 4.2e-32;
Matches 87; Conservative 46; Mismatches 78; Indels 4; Gaps 4;
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Db 24 AVDSVDLTIEKGVDYGVYGVGAGKSTLVRVMNLLQKPTAGEVIVNQTNLSQLSP-KELR 82
Qy 82 QIRKQVGLVFQFAENQIFFEETVLKDVAFGPQNFVSEEDAVKTAAREKALVGDIDESLFDR 141
Db 83 KERKAIGWIFQHP-NLMESRTIPDNVDFSLKYSKSKQERRQKVNELLELVGLEKA-SA 140
Qy 142 SPPELSGGQWRVAIAGILAMEPAAILVLDPTAGLDPLGRKELMTLPKKLH-QSGMTIVL 200
Db 141 YPKQLSGGQQRVAIARALANEPKVLCDDEATSDLPKTTLQILALIKLNRQLGLTIVL 200
Qy 201 VTHLMDVAVYANQVYVMEKGRLVKGGKPSDVFD 235

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OM protein - protein search, using sw model

Run on: October 28, 2005, 17:53:53 ; Search time 167 Seconds
(without alignments)
646.145 Million cell updates/sec

Title: US-09-769-744D-26

Perfect score: 279

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Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	279	100.0	279	3	AY81709 Streptococcus
2	279	100.0	279	6	ABU02751 S. pneumoniae
3	267	95.7	279	4	AM01016 CFE 15 pr
4	267	95.7	279	8	ADK47865 Streptococcus
5	267	95.7	279	8	ADR96203 Novel S.
6	167	59.9	279	4	AU37847 Streptococcus
7	167	59.9	279	6	ABU46314 Protein e
8	23	8.2	288	5	AB53584 Lactococcus
9	22	7.9	279	8	ADK99877 Streptococcus
10	22	7.9	279	8	ADK99878 Streptococcus
11	22	7.9	279	8	ADK99876 Streptococcus
12	22	7.9	279	8	ADK99880 Streptococcus
13	22	7.9	279	8	ADK99881 Streptococcus
14	22	7.9	279	8	ADK99883 Streptococcus
15	22	7.9	279	8	ADK99885 Streptococcus
16	22	7.9	279	8	ADK99879 Streptococcus
17	22	7.9	279	8	ADK99884 Streptococcus
18	22	7.9	279	8	ADK99882 Streptococcus
19	22	7.9	280	5	ABP26998 Streptococcus
20	22	7.9	280	5	ABP26997 Streptococcus
21	22	7.9	280	6	ABU46897 Protein e
22	22	7.9	280	6	ABU44574 Protein e
23	22	7.9	280	6	ADK99875 Streptococcus
24	19	6.8	276	8	AD44624 Bacterial
25	18	6.5	180	2	AAW44388 Vancocycl

ABU17390	Protein e
ADC96403	E. faeciu
AB47921	Listeria
ABU32554	Protein e
ABU29735	Protein e
ABU18769	Protein e
AU34952	Enterococ
ABU29324	Protein e
ADH86847	Enterococ
AD28072	Bacterial
AD06402	Allioiococ
AD06404	Allioiococ
AD24767	Protein e
AD44456	Bacterial
AD43421	Protein e
ABU25566	Protein e
ABU25556	Protein e
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ABU24859	Protein e
AD74754	Murine dn
AAM93187	Human pro
AD130526	Human pro
AAM57027	Propionib
ADMS5546	Propionib
ABU1759	Human MDD
AD55361	Human pro
ADP99144	Human tra
AD13323	Human tra
ABG02184	Novel hum
ADP70147	Human NOV
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AB81576	Human ATP
AB81582	Human ABC
AB84638	Human ABC
AU42362	Propionib
ADMS9481	Propionib
ADP01284	Human ORF
AB61432	ABC trans
AB40367	Human ABC
AB39740	HMM deriv
AD65524	ATP-bindi
AU30609	Klebsiell
ADN26297	Bacterial
ADN26326	Bacterial
ABU31150	Protein e
AB47338	Listeria
ABU45046	Protein e
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ABU43237	Protein e
ABU24072	Protein e
ABP38447	Staphyloc
ABU25536	Protein e
AD807134	Staphyloc
AAB76685	Corynebac
AAG92000	C glutami
ABU43596	Protein e
ABU16367	Protein e
ABU35573	Protein e
ADN26970	Bacterial
AU59476	Propionib
ABM55995	Propionib
AU47175	Propionib
ABM43694	Propionib
ABU48971	Protein e
AD27560	Bacterial
AD28154	Bacterial
ABO72839	Pseudomon
AD13002	TRICH-25.
ABM5034	Human dia
ABP56905	Human dia
AB81577	Human ATP
ABP56906	Human ABC

99	10	3.6	1543	8	ADN33167	Adn33167 Human tra	172	8	2.9	269	4	AAU65782	Aau65782 Propionib
100	10	3.6	1547	5	AAE21168	Aae21168 Human TRI	173	8	2.9	269	6	ABM62301	Abm62301 Propionib
101	10	3.6	1580	5	ABB81581	Abb81581 Human ABC	174	8	2.9	273	4	AAU58254	Aau58254 Propionib
102	10	3.6	1581	5	ABP52097	Abp52097 Homo sapi	175	8	2.9	273	6	ABM54773	Abm54773 Propionib
103	10	3.6	1581	6	ABR44434	Abra44434 Drug tran	176	8	2.9	274	5	ABB48488	Abb48488 Listeria
104	10	3.6	1581	6	ADN04072	Adn04072 Antipsori	177	8	2.9	274	6	ABU32918	Abu32918 Protein e
105	10	3.6	1581	8	ADR99166	Adr99166 ATP-bindi	178	8	2.9	297	8	ADN21934	Adn21934 Bacterial
106	10	3.6	1592	5	AAE21161	Aae21161 Human TRI	179	8	2.9	298	8	ADN25944	Adn25944 Bacterial
107	10	3.6	1595	5	ADH48754	Adh48754 NOV14 pro	180	8	2.9	300	8	ADN24691	Adn24691 Bacterial
108	10	3.6	1621	6	ADA20301	Ada20301 Human ATP	181	8	2.9	306	8	ADS29019	Ads29019 Bacterial
109	10	3.6	1621	8	ABM85036	Abm85036 Human dia	182	8	2.9	319	3	AAU17367	Aau17367 Arabidops
110	10	3.6	1621	8	ADS13000	Ads13000 TRICH-23	183	8	2.9	327	3	AAU17366	Aau17366 Arabidops
111	10	3.6	1633	8	ADS10485	Ads10485 Human the	184	8	2.9	342	3	AAU17365	Aau17365 Arabidops
112	9	3.2	41	6	ABU44072	Abu44072 Protein e	185	8	2.9	378	8	ADK47009	Adk47009 Streptoco
113	9	3.2	196	8	ADS30081	Ads30081 Bacterial	186	8	2.9	380	8	ADN26984	Adn26984 Bacterial
114	9	3.2	273	4	AAU34054	Aau34054 Staphyloc	187	8	2.9	384	5	ABP28071	Abp28071 Streptoco
115	9	3.2	283	6	ABU18623	Abu18623 Protein e	188	8	2.9	384	5	ABP26058	Abp26058 Streptoco
116	9	3.2	284	7	ADE86092	Ade86092 Streptomy	189	8	2.9	384	8	ADN26231	Adn26231 Bacterial
117	9	3.2	285	6	ABU24825	Abu24825 Protein e	190	8	2.9	385	6	ABU01832	Abu01832 S. pneumo
118	9	3.2	285	8	ADN18357	Adn18357 Bacterial	191	8	2.9	385	8	ADR95135	Adr95135 Novel S.
119	9	3.2	286	4	AAU36641	Aau36641 Staphyloc	192	8	2.9	386	3	AAU81644	Aau81644 Streptoco
120	9	3.2	286	6	ABU16471	Abu16471 Protein e	193	8	2.9	428	5	ABB54480	Abb54480 Lactococc
121	9	3.2	286	6	ABM73355	Abm73355 Staphyloc	194	8	2.9	433	6	ADN12523	Adn12523 Alloioccc
122	9	3.2	288	8	ADS28106	Ads28106 Bacterial	195	8	2.9	475	2	AAU08961	Aau08961 A. gossyp
123	9	3.2	290	6	ABU17448	Abu17448 Protein e	196	8	2.9	475	7	ADC94239	Adc94239 E. faeciu
124	9	3.2	292	8	ADS21825	Ads21825 Bacterial	197	8	2.9	479	8	ADS28930	Ads28930 Bacterial
125	9	3.2	294	8	ADS28038	Ads28038 Bacterial	198	8	2.9	506	6	ABU48982	Abu48982 Protein e
126	9	3.2	298	6	ABU25283	Abu25283 Protein e	199	8	2.9	511	8	ADS21343	Adn21343 Bacterial
127	9	3.2	302	4	AAU93108	Aau93108 C glutami	200	8	2.9	530	6	ADN12521	Adn12521 Alloioccc
128	9	3.2	345	8	ADT91429	Adt91429 Arabidops	201	8	2.9	538	4	AAU81583	Aau81583 S. epider
129	9	3.2	346	7	ABO63110	Abu63110 Klebsiell	202	8	2.9	543	6	ABM72610	Abm72610 Staphyloc
130	9	3.2	554	8	ADN17462	Adn17462 Bacterial	203	8	2.9	549	6	ABU22233	Abu22233 Protein e
131	9	3.2	565	5	ABB53631	Abb53631 Lactococc	204	8	2.9	555	2	AAW89799	Aaw89799 Staphyloc
132	9	3.2	579	4	ABG34250	Abg34250 Novel hum	205	8	2.9	560	6	ABM47265	Abm47265 Enterococ
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134	9	3.2	593	8	ADN18083	Adn18083 Bacterial	207	8	2.9	561	5	ADN27155	Adn27155 Bacterial
135	9	3.2	595	6	ABM70715	Abm70715 Phototrab	208	8	2.9	567	8	ABP40801	Abp40801 Staphyloc
136	9	3.2	595	7	ADP05723	Adp05723 Bacterial	209	8	2.9	567	8	ADS08129	Ads08129 Staphyloc
137	9	3.2	605	8	ADN19948	Adn19948 Bacterial	210	8	2.9	568	6	ABM65635	Abm65635 Propionib
138	9	3.2	611	5	ABB53567	Abb53567 Lactococc	211	8	2.9	572	6	ADN12519	Adn12519 Alloioccc
139	9	3.2	611	8	ADS29283	Ads29283 Bacterial	212	8	2.9	574	6	ADN12517	Adn12517 Alloioccc
140	9	3.2	686	7	ABO66990	Abu66990 Klebsiell	213	8	2.9	575	8	ADS29807	Ads29807 Bacterial
141	9	3.2	800	8	ADN25664	Adn25664 Bacterial	214	8	2.9	576	8	ADS30944	Ads30944 Bacterial
142	9	3.2	950	6	ABU19361	Abu19361 Protein e	215	8	2.9	583	4	AAU37865	Aau37865 Streptoco
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144	9	3.2	1105	8	ADS42794	Ads42794 Bacterial	217	8	2.9	583	6	ABU46225	Abu46225 Streptoco
145	9	3.2	1164	8	ADN27117	Adn27117 Bacterial	218	8	2.9	583	6	ABU46225	Abu46225 Protein e
146	9	3.2	1182	6	ABU25521	Abu25521 Protein e	219	8	2.9	586	6	ADB09066	Adb09066 Alloioccc
147	8	2.9	76	8	ABO57090	Abu57090 Human gen	220	8	2.9	596	7	ADH86631	Adh86631 Enterococ
148	8	2.9	119	8	ADS28727	Ads28727 Bacterial	221	8	2.9	601	5	ABB48195	Abb48195 Listeria
149	8	2.9	129	2	AAW27793	Aaw27793 Amino aci	222	8	2.9	606	4	ABB59933	Abb59933 Drosophil
150	8	2.9	202	5	ABG34149	Abg34149 Human lun	223	8	2.9	608	5	ABB54609	Abb54609 Lactococc
151	8	2.9	212	4	AAU65505	Aau65505 Propionib	224	8	2.9	608	8	ADS29389	Ads29389 Bacterial
152	8	2.9	212	6	ABM62024	Abm62024 Propionib	225	8	2.9	624	8	ADS27378	Ads27378 Bacterial
153	8	2.9	215	2	AAU93246	Aau93246 Mouse int	226	8	2.9	642	4	AAU56693	Aau56693 Propionib
154	8	2.9	215	2	AAW44004	Aaw44004 Murine in	227	8	2.9	642	6	ABP79387	Abp79387 N. gonorr
155	8	2.9	215	2	AAW56711	Aaw56711 p40 subun	228	8	2.9	642	6	ABM53212	Abm53212 Propionib
156	8	2.9	215	6	ABU10115	Abu10115 Mouse int	229	8	2.9	642	6	ABU37367	Abu37367 Protein e
157	8	2.9	225	6	ABM70650	Abm70650 Phototrab	230	8	2.9	646	2	AAU36926	Aau36926 Amino aci
158	8	2.9	237	8	ADN18257	Adn18257 Bacterial	231	8	2.9	646	5	ABB94344	Abb94344 Chlamydia
159	8	2.9	243	4	AAU76693	Aau76693 Corynebac	232	8	2.9	647	8	ABU27271	Abu27271 Protein e
160	8	2.9	243	4	AAU91098	Aau91098 C glutami	233	8	2.9	650	5	ABB48907	Abb48907 Listeria
161	8	2.9	243	8	ADQ59493	Adq59493 Human can	234	8	2.9	650	6	ABU32711	Abu32711 Protein e
162	8	2.9	248	8	ADN18335	Adn18335 Bacterial	235	8	2.9	673	8	ADS28635	Ads28635 Bacterial
163	8	2.9	250	5	ABP26471	Abp26471 Streptoco	236	8	2.9	674	8	ADN28161	Adn28161 Bacterial
164	8	2.9	255	5	ABP62780	Abp62780 Protein f	237	8	2.9	690	8	ADN19274	Adn19274 Bacterial
165	8	2.9	255	7	ADU72191	Adu72191 S. roseosp	238	8	2.9	810	5	ABP65287	Abp65287 Bifidobac
166	8	2.9	258	5	ABB53634	Abb53634 Lactococc	239	8	2.9	1117	8	ADS41743	Ads41743 Bacterial
167	8	2.9	259	5	ABB55099	Abb55099 Lactococc	240	8	2.9	1167	8	ADS22896	Ads22896 Bacterial
168	8	2.9	263	8	ADK46499	Adk46499 Streptoco	241	8	2.9	1199	8	ADN27260	Adn27260 Bacterial
169	8	2.9	264	8	ADR94449	Adr94449 Novel S.	242	8	2.9	1511	4	ABB58545	Abb58545 Drosophil
170	8	2.9	267	4	AAU56319	Aau56319 Propionib	243	8	2.9	2580	4	ABB66260	Abb66260 Drosophil
171	8	2.9	267	6	ABM52838	Abm52838 Propionib	244	7	2.5	7	2	AAW44377	Aaw44377 Vancomyci

245	7	2.5	8	4	AAJ02868	AaJ02868	Hepatitis	318	7	2.5	142	3	AAAB19730	Aab19730	Human SEC
246	7	2.5	8	4	AAJ02505	AaJ02505	Hepatitis	319	7	2.5	142	7	ADK18307	Adk18307	Human mol
247	7	2.5	8	4	AAJ00504	AaJ00504	Hepatitis	320	7	2.5	142	7	ADK68142	Adk68142	Novel NOV
248	7	2.5	9	4	AAJ00789	AaJ00789	Hepatitis	321	7	2.5	142	7	ADK68138	Adk68138	Novel NOV
249	7	2.5	9	4	AAJ02814	AaJ02814	Hepatitis	322	7	2.5	142	7	ADQ95880	Adq95880	T cell ac
250	7	2.5	9	4	AAJ02414	AaJ02414	Hepatitis	323	7	2.5	142	8	ADR49127	Adr49127	Human NOV
251	7	2.5	9	5	AAJ00077	AaJ00077	HCV NG3 h	324	7	2.5	142	8	ADR49131	Adr49131	Human NOV
252	7	2.5	10	4	AAJ00342	AaJ00342	Hepatitis	325	7	2.5	145	4	AAJ04987	Aam4987	Human rep
253	7	2.5	10	4	AAJ01508	AaJ01508	Hepatitis	326	7	2.5	145	4	ABB95695	Abb95695	Human tes
254	7	2.5	10	4	AAJ00505	AaJ00505	Hepatitis	327	7	2.5	148	6	ADA36713	Ada36713	Acinetoba
255	7	2.5	11	4	AAJ00753	AaJ00753	Hepatitis	328	7	2.5	149	6	ABM69510	Abm69510	Photorhab
256	7	2.5	11	4	AAJ01094	AaJ01094	Hepatitis	329	7	2.5	151	8	ADR32314	Adr32314	Renilla r
257	7	2.5	11	4	AAJ02506	AaJ02506	Hepatitis	330	7	2.5	152	8	ADR32312	Adr32312	Renilla r
258	7	2.5	11	4	AAJ02717	AaJ02717	Hepatitis	331	7	2.5	157	2	AAW33886	Aaw33886	Flea sali
259	7	2.5	11	4	AAJ02236	AaJ02236	Hepatitis	332	7	2.5	157	2	AAW82360	Aaw82360	Flea sali
260	7	2.5	11	4	AAJ01939	AaJ01939	Hepatitis	333	7	2.5	157	2	AAW82360	Aaw82360	Flea sali
261	7	2.5	15	8	ADL26022	Adl26022	Synthetic	334	7	2.5	158	5	AAU30886	Aau30886	Novel hum
262	7	2.5	15	8	ADL25996	Adl25996	Synthetic	335	7	2.5	161	8	ADN47187	Adn47187	Thermococ
263	7	2.5	15	8	ADL25997	Adl25997	Synthetic	336	7	2.5	166	4	AAU00974	Aau00974	Human bon
264	7	2.5	15	8	ADL25999	Adl25999	Synthetic	337	7	2.5	174	6	ABU01226	Abu01226	S. pneumo
265	7	2.5	15	8	ADL26000	Adl26000	Synthetic	338	7	2.5	176	4	AAU18425	Aau18425	Human imm
266	7	2.5	15	8	ADL25995	Adl25995	Synthetic	339	7	2.5	176	4	AAU18425	Aau18425	Human end
267	7	2.5	15	8	ADL26025	Adl26025	Synthetic	340	7	2.5	176	8	ADS21408	Ads21408	Bacterial
268	7	2.5	15	8	ADL25998	Adl25998	Synthetic	341	7	2.5	185	2	AAU02369	Aau02369	Polypepti
269	7	2.5	15	8	ADL26023	Adl26023	Synthetic	342	7	2.5	187	5	ABP03719	Abp03719	Human ORF
270	7	2.5	15	8	ADL26024	Adl26024	Synthetic	343	7	2.5	189	7	ADF07647	Adf07647	Bacterial
271	7	2.5	15	8	ADL26026	Adl26026	Synthetic	344	7	2.5	189	8	ADN26887	Adn26887	Bacterial
272	7	2.5	15	8	ADL26027	Adl26027	Synthetic	345	7	2.5	192	6	ADB17009	Adb17009	ABC trans
273	7	2.5	18	2	AAU13344	Aau13344	HCV	346	7	2.5	193	4	AAU13344	Aau13344	S. epider
274	7	2.5	18	2	AAU13344	Aau13344	HCV	347	7	2.5	194	5	ABW77262	Abw77262	HCV bait
275	7	2.5	20	8	ADM23867	Adm23867	Polypepti	348	7	2.5	197	4	AAU18425	Aau18425	Corynebac
276	7	2.5	20	8	ADM29123	Adm29123	Hepatitis	349	7	2.5	197	8	ADS44690	Ads44690	Bacterial
277	7	2.5	24	2	AAU60137	Aau60137	Mycobacte	350	7	2.5	198	7	ABO63975	Abu63975	Klebsiell
278	7	2.5	24	2	AAU14884	Aau14884	N-termina	351	7	2.5	202	6	ABU21011	Abu21011	Protein e
279	7	2.5	24	5	ABW73490	Abw73490	M. vaccae	352	7	2.5	202	6	ABU21011	Abu21011	Protein e
280	7	2.5	28	5	ABW77227	Abw77227	Selected	353	7	2.5	205	4	AAU03136	Aau03136	Streptoco
281	7	2.5	30	5	AAU84680	Aau84680	HCV HepC1	354	7	2.5	207	2	AAU25859	Aau25859	HCV polyp
282	7	2.5	30	5	AAU84679	Aau84679	HCV HepC1	355	7	2.5	207	2	AAU25859	Aau25859	HCV polyp
283	7	2.5	34	8	ADI34965	Adi34965	Hepatitis	356	7	2.5	208	8	AAW41737	Aaw41737	Hepatitis
284	7	2.5	40	2	AAU51162	Aau51162	Peptide (357	7	2.5	213	2	AAU20717	Aau20717	C10-23 NA
285	7	2.5	41	8	ADL26412	Adl26412	Synthetic	358	7	2.5	213	2	AAU20717	Aau20717	C10-23 NA
286	7	2.5	41	8	ADL26413	Adl26413	Synthetic	359	7	2.5	213	2	AAU20717	Aau20717	C10-23 NA
287	7	2.5	43	8	ADS05293	Ads05293	Staphyloc	360	7	2.5	216	6	ABM65399	Abm65399	Propionib
288	7	2.5	49	2	AAU33866	Aau33866	Polypepti	361	7	2.5	220	8	ADN26973	Adn26973	Bacterial
289	7	2.5	50	2	AAU33350	Aau33350	Novel hum	362	7	2.5	221	6	AAU25881	Aau25881	HK6, 9/20
290	7	2.5	67	4	ABG01599	Abg01599	Novel hum	363	7	2.5	221	6	AAU25881	Aau25881	HK6, 9/20
291	7	2.5	70	5	ABP10464	Abp10464	Human ORF	364	7	2.5	222	6	ABP81430	Abp81430	Streptoco
292	7	2.5	71	3	AAU00410	Aau00410	Human sec	365	7	2.5	223	4	AAU00410	Aau00410	Human sec
293	7	2.5	72	3	AAU65113	Aau65113	Human 5'	366	7	2.5	224	2	AAW80708	Aaw80708	S. pneumo
294	7	2.5	80	2	AAU04874	Aau04874	DNA fragm	367	7	2.5	228	6	ABU37611	Abu37611	Protein e
295	7	2.5	82	2	AAW24596	Aaw24596	Hepatitis	368	7	2.5	228	6	ABU37611	Abu37611	Protein e
296	7	2.5	82	2	AAW44815	Aaw44815	Hepatitis	369	7	2.5	228	6	ABU37611	Abu37611	Protein e
297	7	2.5	84	5	ABP05993	Abp05993	Human ORF	370	7	2.5	229	2	AAU98349	Aau98349	Novel S.
298	7	2.5	88	7	ADP089170	Adp089170	Ribosomal	371	7	2.5	230	8	ADN17519	Adn17519	Bacterial
299	7	2.5	89	8	ADS30531	Ads30531	Bacterial	372	7	2.5	232	6	ABM71118	Abm71118	Staphyloc
300	7	2.5	98	3	AAU65425	Aau65425	Human 5'	373	7	2.5	232	6	ABM71118	Abm71118	Staphyloc
301	7	2.5	102	4	AAU67310	Aau67310	ABC trans	374	7	2.5	233	3	AAU75763	Aau75763	Neisseria
302	7	2.5	102	4	AAU45738	Aau45738	Propionib	375	7	2.5	233	3	AAU75763	Aau75763	Neisseria
303	7	2.5	102	6	ABM42257	Abm42257	Propionib	376	7	2.5	233	8	ADL05394	Adl05394	M. catarr
304	7	2.5	108	7	ADP36598	Adp36598	Human NOV	377	7	2.5	233	8	ADL05394	Adl05394	M. catarr
305	7	2.5	109	7	ADP36598	Adp36598	Human NOV	378	7	2.5	235	5	ABP30426	Abp30426	Bacterial
306	7	2.5	109	7	ADP36598	Adp36598	Human NOV	379	7	2.5	235	6	ABU42193	Abu42193	Protein e
307	7	2.5	111	3	AAU65371	Aau65371	Human 5'	380	7	2.5	235	6	ABU42193	Abu42193	Protein e
308	7	2.5	112	3	AAU15670	Aau15670	Arabisops	381	7	2.5	235	7	ADM26338	Adm26338	Hyperther
309	7	2.5	114	4	AAU31975	Aau31975	Novel hum	382	7	2.5	235	8	ADS30303	Ads30303	Bacterial
310	7	2.5	116	4	ABG04902	Abg04902	Novel hum	383	7	2.5	237	6	ADL12443	Adl12443	Alloioococ
311	7	2.5	117	6	ADA77747	Ada77747	Partial:s	384	7	2.5	237	6	ADL12443	Adl12443	Alloioococ
312	7	2.5	121	7	ADK68144	Adk68144	Novel NOV	385	7	2.5	246	1	AAU92030	Aau92030	Sequence
313	7	2.5	121	8	ADR49133	Adr49133	Human NOV	386	7	2.5	246	6	ABU21727	Abu21727	Protein e
314	7	2.5	125	2	AAU12263	Aau12263	Human 5'	387	7	2.5	247	6	AAU92340	Aau92340	C. glutami
315	7	2.5	125	7	ADD18252	Add18252	Human mol	388	7	2.5	251	5	ABP65924	Abp65924	Bifidobac
316	7	2.5	125	7	ADK68140	Adk68140	Novel NOV	389	7	2.5	251	6	ADL12441	Adl12441	Alloioococ
317	7	2.5	125	8	ADR49129	Adr49129	Human NOV	390	7	2.5	251	7	ADF04354	Adf04354	Bacterial
					ADA55239	Ada55239	Human pro								

391	7	2.5	252	4	AAM86393	Human imm	464	7	2.5	280	5	ABP38624	Staphyloc
392	7	2.5	252	4	AAM91743	Human imm	465	7	2.5	280	8	ADS05124	Staphyloc
393	7	2.5	252	4	AAM42386	Human pol	466	7	2.5	281	2	AAV37001	Chlamydia
394	7	2.5	252	4	AAU18422	Human end	467	7	2.5	281	6	ABU01985	S. pneumo
395	7	2.5	252	4	AAU18423	Human end	468	7	2.5	281	7	ADH86577	Enterococ
396	7	2.5	252	4	ABO67564	Klebsiell	469	7	2.5	282	2	AAW01956	Hepatit
397	7	2.5	253	2	AAAR20609	Cil-7 NAN	470	7	2.5	282	6	ABP70431	Amino aci
398	7	2.5	253	2	AAR60321	NANBH vir	471	7	2.5	282	2	ABO62850	Klebsiell
399	7	2.5	253	8	ADN46403	Thermococ	472	7	2.5	284	2	AAR20614	C10-16 NA
400	7	2.5	257	4	ABBS8273	Drosophil	473	7	2.5	284	2	AAR50071	NANBH vir
401	7	2.5	258	8	ADBS29521	Bacterial	474	7	2.5	284	2	AAV34801	Chlamydia
402	7	2.5	259	7	ADP06451	Bacterial	475	7	2.5	284	8	ADJ181676	Non-A-non
403	7	2.5	260	8	ADN22410	Bacterial	476	7	2.5	285	4	AAW67316	Gene #2 p
404	7	2.5	261	4	AAU18298	Human end	477	7	2.5	285	6	ABU24615	Protein e
405	7	2.5	261	6	ABM71008	Staphyloc	478	7	2.5	286	2	AAR40222	Hepatit
406	7	2.5	263	5	ABW77261	HCV bait	479	7	2.5	290	5	ABP38428	Staphyloc
407	7	2.5	263	7	ADE36629	Human NOV	480	7	2.5	290	8	ADSO7099	Adso7099
408	7	2.5	263	7	ADE36622	Plasmid p	481	7	2.5	291	6	ADA77739	Wild type
409	7	2.5	263	7	ADE36596	Human NOV	482	7	2.5	291	7	ADC94578	E. faeciu
410	7	2.5	266	1	AAP90147	Sequence	483	7	2.5	291	8	ADS30591	Bacterial
411	7	2.5	266	1	AAR62863	Korean-ty	484	7	2.5	292	6	ADA33607	Acinetoba
412	7	2.5	266	2	AAR90932	HCV anti	485	7	2.5	293	4	ABP79182	Corynebac
413	7	2.5	266	2	AAR90932	HCV anti	486	7	2.5	293	4	AAV91103	C glutami
414	7	2.5	266	5	ABP25447	Sreptoco	487	7	2.5	293	5	ABP26437	Sreptoco
415	7	2.5	267	6	ABM68503	Phototrab	488	7	2.5	293	7	ADL65435	C. Glutam
416	7	2.5	267	8	ADI39249	S. hygro	489	7	2.5	294	3	AAV69849	Hepatit
417	7	2.5	269	4	AAU66854	Propionib	490	7	2.5	294	6	ABU48972	Protein e
418	7	2.5	269	6	ABM63373	Propionib	491	7	2.5	295	6	ABR63601	Hepatit
419	7	2.5	269	6	ABU43238	Protein e	492	7	2.5	295	6	ABR63601	Hepatit
420	7	2.5	269	6	ABU16230	Protein e	493	7	2.5	297	8	ADS22519	Bacterial
421	7	2.5	270	6	ADA77740	Regions o	494	7	2.5	297	8	ADN27327	Bacterial
422	7	2.5	272	2	AAR14545	Encoded b	495	7	2.5	298	6	ABU41764	Protein e
423	7	2.5	272	2	AAR14356	HCV prote	496	7	2.5	298	8	ADQ76693	Human KIM
424	7	2.5	272	2	AAR68546	Hepatit	497	7	2.5	298	8	ADS27088	Bacterial
425	7	2.5	272	2	AAR68546	Hepatit	498	7	2.5	298	8	ADQ41991	Bacterial
426	7	2.5	272	2	AAW46396	Amino aci	499	7	2.5	299	2	AAW68549	Hepatit
427	7	2.5	272	2	AAW97608	Amino aci	500	7	2.5	299	2	AAW68549	Hepatit
428	7	2.5	272	6	ABO27019	Hepatit	501	7	2.5	299	2	AAW01699	Protein d
429	7	2.5	272	6	ADA07873	Hepatit	502	7	2.5	299	2	AAW01699	Protein d
430	7	2.5	273	2	AAR50072	NANBH vir	503	7	2.5	299	2	AAW46386	Protease
431	7	2.5	273	5	ABP38796	Staphyloc	504	7	2.5	299	2	AAW97598	Protein s
432	7	2.5	274	8	ADJ81677	Non-A-non	505	7	2.5	299	2	AAW97598	Protein s
433	7	2.5	274	4	AAU34053	Staphyloc	506	7	2.5	299	6	ABO27063	Hepatit
434	7	2.5	274	6	ABU36368	Protein e	507	7	2.5	299	6	ABO27063	Hepatit
435	7	2.5	274	6	ABU35572	Protein e	508	7	2.5	299	8	ADA07942	Hepatit
436	7	2.5	275	6	ADA33530	Acinetoba	509	7	2.5	300	3	AAV69648	Bacterial
437	7	2.5	277	4	AAU43271	Propionib	510	7	2.5	300	6	ABM68949	Phototrab
438	7	2.5	277	6	ABM39790	Propionib	511	7	2.5	300	7	ADH85848	Enterococ
439	7	2.5	277	6	ABU25559	Protein e	512	7	2.5	300	8	ADSO15292	Hepatit
440	7	2.5	278	2	AAR84358	Hepatit	513	7	2.5	300	8	ADS23576	Bacterial
441	7	2.5	278	5	ABW77259	HCV bait	514	7	2.5	300	8	ADS28908	Bacterial
442	7	2.5	278	6	ABU27455	Protein e	515	7	2.5	301	2	AAW01049	Product o
443	7	2.5	278	8	ADSO15289	Hepatit	516	7	2.5	301	3	AAV97058	Human T h
444	7	2.5	279	3	AAV43883	Amino aci	517	7	2.5	301	3	AAV97058	Human T h
445	7	2.5	279	3	AAV43892	Amino aci	518	7	2.5	301	4	AAW51104	Human 200
446	7	2.5	279	3	AAV43893	Amino aci	519	7	2.5	301	4	AAW51104	Human 200
447	7	2.5	279	3	AAV43880	Amino aci	520	7	2.5	301	4	AAW50223	Human 200
448	7	2.5	279	3	AAV43881	Amino aci	521	7	2.5	301	4	AAW50223	Human 200
449	7	2.5	279	3	AAV43886	Amino aci	522	7	2.5	301	4	AAW51104	Human 200
450	7	2.5	279	3	AAV43878	Amino aci	523	7	2.5	301	4	AAW51104	Human 200
451	7	2.5	279	3	AAV43891	Amino aci	524	7	2.5	301	4	AAW50223	Human 200
452	7	2.5	279	3	AAV43887	Amino aci	525	7	2.5	301	4	AAW50223	Human 200
453	7	2.5	279	3	AAV43884	Amino aci	526	7	2.5	301	4	AAW50223	Human 200
454	7	2.5	279	3	AAV43879	Amino aci	527	7	2.5	301	4	AAW50223	Human 200
455	7	2.5	279	3	AAV43888	Amino aci	528	7	2.5	301	4	AAW50223	Human 200
456	7	2.5	279	3	AAV43889	Amino aci	529	7	2.5	301	4	AAW50223	Human 200
457	7	2.5	279	3	AAV43882	Amino aci	530	7	2.5	301	4	AAW50223	Human 200
458	7	2.5	279	4	ABG25857	Novel hum	531	7	2.5	301	7	ABR82713	Human TIM
459	7	2.5	279	5	ABBA7922	Listeria	532	7	2.5	301	7	ABR82713	Human TIM
460	7	2.5	279	6	ABU32730	Protein e	533	7	2.5	301	8	ADH80727	Human pol
461	7	2.5	279	6	ABU24207	Protein e	534	7	2.5	301	8	ADQ95878	Human PRO
462	7	2.5	279	6	ADB06406	Alloecoc	535	7	2.5	301	8	ADQ95876	T cell ac
463	7	2.5	280	4	AAB96282	Putative	536	7	2.5	302	8	ADN26506	Bacterial

537	7	2.5	302	8	ADS25912	Adg25912 Bacterial
538	7	2.5	304	6	ABM67587	ABM67587 Phototab
539	7	2.5	304	8	ADS26336	Adg26336 Bacterial
540	7	2.5	304	8	ADS41984	Adg41984 Bacterial
541	7	2.5	304	8	ADS26703	Adg26703 Bacterial
542	7	2.5	305	6	ABP70430	ABP70430 Amino aci
543	7	2.5	306	4	AAU36640	AAU36640 Staphyloc
544	7	2.5	306	4	ABB62221	ABb62221 Drosophil
545	7	2.5	306	6	ABM73365	ABM73365 Staphyloc
546	7	2.5	306	8	ADN26437	ADN26437 Bacterial
547	7	2.5	306	8	ADS23044	Adg23044 Bacterial
548	7	2.5	307	2	AAAR29859	AAr29859 HCV NS2-N
549	7	2.5	307	2	AAAR29858	AAr29858 HCV NS2-N
550	7	2.5	307	2	AAAR29857	AAr29857 HCV NS2-N
551	7	2.5	307	2	AAAR29843	AAr29843 HCV NS2-N
552	7	2.5	307	2	AAAR29843	AAr29843 Rat kidne
553	7	2.5	307	4	AAW38334	AAw38334 Putative
554	7	2.5	307	6	ABU38602	ABu38602 Protein e
555	7	2.5	307	4	AAU34619	AAu34619 E. coli c
556	7	2.5	308	4	AAU98922	AAu98922 B. coli g
557	7	2.5	308	4	AAU29364	AAu29364 Novel mar
558	7	2.5	308	6	ABU28679	ABu28679 Protein e
559	7	2.5	308	6	ABU47287	ABu47287 Protein e
560	7	2.5	308	8	ADN17599	ADn17599 Bacterial
561	7	2.5	308	8	ADN24970	ADn24970 Bacterial
562	7	2.5	308	8	ADN23041	ADn23041 Bacterial
563	7	2.5	308	8	ADN18052	ADn18052 Bacterial
564	7	2.5	308	8	ADN18240	ADn18240 Bacterial
565	7	2.5	309	7	ABO72458	ABo72458 Pseudomon
566	7	2.5	309	8	ADN22211	ADn22211 Bacterial
567	7	2.5	309	8	ADN22487	ADn22487 Bacterial
568	7	2.5	310	8	ADM94402	ADM94402 Wheat MRP
569	7	2.5	311	2	AAAR27165	AAr27165 Recombina
570	7	2.5	311	2	AAAR48550	AAr48550 Recombina
571	7	2.5	311	2	AAAR74079	AAr74079 Renilla r
572	7	2.5	311	2	AAAY39947	AAy39947 R. muller
573	7	2.5	311	3	AAAY84836	AAy84836 Amino aci
574	7	2.5	311	3	AAAY70363	AAy70363 Renilla l
575	7	2.5	311	3	AAAY44791	AAy44791 Soybean A
576	7	2.5	311	3	AAAG46265	AAg46265 Arabidops
577	7	2.5	311	3	ABBA47282	ABb47282 Enterococ
578	7	2.5	311	4	AAE13381	AAe13381 Renilla m
579	7	2.5	311	5	AAE19116	AAe19116 Renilla r
580	7	2.5	311	5	AAE19115	AAe19115 Renilla r
581	7	2.5	311	5	AAU11515	AAu11515 Renilla l
582	7	2.5	311	5	ABB97171	ABb97171 R renifor
583	7	2.5	311	5	ABB97172	ABb97172 R renifor
584	7	2.5	311	5	ABB97170	ABb97170 R renifor
585	7	2.5	311	5	ABB97173	ABb97173 R renifor
586	7	2.5	311	5	ABB49854	ABb49854 Listeria
587	7	2.5	311	6	ABU02212	ABu02212 S. pneumo
588	7	2.5	311	6	AAO27521	AAo27521 Renilla (
589	7	2.5	311	6	ADK46590	ADk46590 Streptoco
590	7	2.5	311	8	ADM94398	ADm94398 Soybean M
591	7	2.5	311	8	ADM94398	ADm94398 Sea pansy
592	7	2.5	312	8	ABU49846	ABu49846 Protein e
593	7	2.5	312	8	ADS25557	ADs25557 Bacterial
594	7	2.5	312	8	AAAR27166	AAr27166 Sequence
595	7	2.5	314	2	AAAR48549	AAr48549 Sequence
596	7	2.5	314	2	AAAR26343	AAr26343 Arabidops
597	7	2.5	314	3	AAAG43058	AAg43058 Arabidops
598	7	2.5	314	3	AAAG28959	AAg28959 Arabidops
599	7	2.5	314	4	AAAB51159	AAb51159 Renilla r
600	7	2.5	314	4	AAAB96594	AAb96594 Putative
601	7	2.5	314	5	ABB82055	ABb82055 R.f reinfo
602	7	2.5	314	5	AAE13366	AAe13366 Renilla r
603	7	2.5	314	5	AAE13366	AAe13366 Renilla r
604	7	2.5	314	5	ABB82041	ABb82041 R. reinfo
605	7	2.5	314	6	ADA14766	ADa14766 Sea pansy
606	7	2.5	314	6	ABG73286	ABg73286 Renilla r
607	7	2.5	314	6	ADA37435	ADa37435 Renilla r
608	7	2.5	314	7	ABW00605	ABw00605 Renilla r
609	7	2.5	314	8	ADM80595	ADM80595 Luciferas

610	7	2.5	314	8	ADR43968	ADR43968 Renilla r
611	7	2.5	314	8	Adg28016	Adg28016 Bacterial
612	7	2.5	314	8	Adg43192	Adg43192 Bacterial
613	7	2.5	314	8	Adg29090	Adg29090 Bacterial
614	7	2.5	314	8	Adg42552	Adg42552 Bacterial
615	7	2.5	315	2	AAAR28466	AAr28466 Sequence
616	7	2.5	315	6	ABU44977	ABu44977 Protein e
617	7	2.5	315	6	ADH88564	ADh88564 Acinetoba
618	7	2.5	315	6	ADH88564	ADh88564 Enterococ
619	7	2.5	315	8	ADR95279	ADR95279 Novel S.
620	7	2.5	315	8	ABRS53222	ABr53222 Protein s
621	7	2.5	316	6	ADFO5899	ADf05899 Bacterial
622	7	2.5	316	7	ADK63718	ADk63718 Disease t
623	7	2.5	316	8	ADK63718	ADk63718 Bacterial
624	7	2.5	316	8	ADs29721	ADs29721 Bacterial
625	7	2.5	316	8	ADs29721	ADs29721 Protein e
626	7	2.5	317	6	ABU42860	ABu42860 Klebsiell
627	7	2.5	317	7	ABO64109	ABo64109 Klebsiell
628	7	2.5	318	3	AAAY43898	AAy43898 Amino aci
629	7	2.5	318	3	AAAY43900	AAy43900 Amino aci
630	7	2.5	318	3	AAAY43899	AAy43899 Amino aci
631	7	2.5	318	3	AAAY43894	AAy43894 Amino aci
632	7	2.5	318	3	AAAY43895	AAy43895 Amino aci
633	7	2.5	318	5	ABP66268	ABp66268 Bifidobac
634	7	2.5	319	5	ABP39043	ABp39043 Staphyloc
635	7	2.5	319	5	ABBS5189	ABb5189 Lactococc
636	7	2.5	319	5	ABBS5242	ABb5242 Lactococc
637	7	2.5	319	6	ABU43920	ABu43920 Protein e
638	7	2.5	319	6	ABO61599	ABo61599 Klebsiell
639	7	2.5	319	8	ADSO7028	ADs07028 Staphyloc
640	7	2.5	323	4	AAAB96077	AAb96077 Putative
641	7	2.5	323	7	ABO65979	ABo65979 Klebsiell
642	7	2.5	324	6	ABM71022	ABm71022 Staphyloc
643	7	2.5	326	3	AAAY43897	AAy43897 Amino aci
644	7	2.5	326	3	AAAY43896	AAy43896 Amino aci
645	7	2.5	326	6	AAAG46264	AAg46264 Arabidops
646	7	2.5	326	6	ABU28141	ABu28141 Protein e
647	7	2.5	327	2	ABO65446	ABo65446 Klebsiell
648	7	2.5	327	2	AAAR41437	AAr41437 PT-NANBH
649	7	2.5	328	5	ABP38817	ABp38817 Staphyloc
650	7	2.5	328	6	ABU15017	ABu15017 Protein e
651	7	2.5	330	2	AAAW26162	AAw26162 Fragment
652	7	2.5	330	8	ADJ56872	ADj56872 Corn TTG
653	7	2.5	330	8	ADs42868	ADs42868 Bacterial
654	7	2.5	333	5	ABBA49315	ABb49315 Listeria
655	7	2.5	333	6	ABU32615	ABu32615 Protein e
656	7	2.5	334	2	AAAW38336	AAw38336 Human kid
657	7	2.5	334	4	AAAB84657	AAb84657 Amino aci
658	7	2.5	334	6	AAO26679	AAo26679 KIM-1 rel
659	7	2.5	334	6	ADQ29371	ADo29371 Mouse GPC
660	7	2.5	334	8	ADQ29371	ADo29371 Bacterial
661	7	2.5	334	8	ADQ76696	ADq76696 Human kid
662	7	2.5	335	3	ABO72091	ABo72091 Pseudomon
663	7	2.5	336	3	AAAG46263	AAg46263 Arabidops
664	7	2.5	336	4	ABG25968	ABg25968 Novel hum
665	7	2.5	338	8	ADM94350	ADm94350 Corn P-gl
666	7	2.5	339	3	AAAY84839	AAy84839 Amino aci
667	7	2.5	339	3	AAAY84839	AAy84839 Amino aci
668	7	2.5	339	3	AAAY84841	AAy84841 Amino aci
669	7	2.5	339	3	AAAY84840	AAy84840 Amino aci
670	7	2.5	339	3	AAAY84837	AAy84837 Human Pro
671	7	2.5	339	7	ADDA6755	ADd46755 Rat Prote
672	7	2.5	339	7	ADDA6755	ADd46755 Rat Prote
673	7	2.5	339	7	ADE55552	ADe55552 Rat Prote
674	7	2.5	339	7	ADE55554	ADe55554 Human Pro
675	7	2.5	339	7	ADs36618	ADs36618 Plasmid p
676	7	2.5	339	7	ADs36592	ADs36592 Human NOV
677	7	2.5	339	8	ADQ17619	ADq17619 Human sof
678	7	2.5	339	8	ABM81054	ABm81054 Tumour-as
679	7	2.5	340	4	AAAG91479	AAg91479 C Glutam
680	7	2.5	341	6	ABU31733	ABu31733 Protein e
681	7	2.5	341	6	ABU14858	ABu14858 Protein e
682	7	2.5	341	6	ABU14858	ABu14858 Protein e

683	7	2.5	343	6	ABU02418	Abu02418 S. pneumo	756	7	2.5	377	6	ABM71759	Abm71759 Staphyloc
684	7	2.5	343	6	ABP81463	Abp81463 Streptococ	757	7	2.5	377	7	ADG30683	Adg30683 Xanthomon
685	7	2.5	344	6	ABU33636	Abu33636 Protein e	758	7	2.5	378	6	ABJ25519	Abj25519 Aspergill
686	7	2.5	344	6	ABU41749	Abu41749 Protein e	759	7	2.5	379	6	ABU17175	Abu17175 Protein e
687	7	2.5	344	6	ABU38248	Abu38248 Protein e	760	7	2.5	381	6	ABU44734	Abu44734 Protein e
688	7	2.5	344	6	ABJ37499	Abj37499 HCV relat	761	7	2.5	383	5	ABU05485	Abu05485 M. tuberc
689	7	2.5	344	8	ADJ56875	Adj56875 Soybean T	762	7	2.5	383	6	ABU35880	Abu35880 Protein e
690	7	2.5	345	6	ABU49126	Abu49126 Protein e	763	7	2.5	383	6	ABU44545	Abu44545 Protein e
691	7	2.5	346	3	AAG26342	Aag26342 Arabidops	764	7	2.5	383	6	ADA34135	Ada34135 Acinetoba
692	7	2.5	346	3	AAG28958	Aag28958 Arabidops	765	7	2.5	385	6	ABU39392	Abu39392 Protein e
693	7	2.5	346	3	AAG43057	Aag43057 Arabidops	766	7	2.5	385	8	ABM82071	Abm82071 Tumour-as
694	7	2.5	346	6	ABM67738	Abm67738 Photorhab	767	7	2.5	391	7	ABM85384	Abm85384 Mouse pro
695	7	2.5	346	8	ADN72745	Adn72745 Thale cre	768	7	2.5	391	8	ADS25330	Ads25330 Bacterial
696	7	2.5	346	8	ADN72435	Adn72435 Thale cre	769	7	2.5	399	8	ADS28526	Ads28526 Bacterial
697	7	2.5	347	6	ABP80915	Abp80915 N. gonorr	770	7	2.5	401	6	ABJ37916	Abj37916 NOVX prot
698	7	2.5	347	6	ABP80525	Abp80525 N. gonorr	771	7	2.5	404	2	AAW98637	Aaw98637 H. pylori
699	7	2.5	347	6	ABU37729	Abu37729 Protein e	772	7	2.5	408	6	ABP80531	Abp80531 N. gonorr
700	7	2.5	347	6	ABU37572	Abu37572 Protein e	773	7	2.5	408	6	ABP80918	Abp80918 N. gonorr
701	7	2.5	347	8	ADP08174	Adp08174 Neisseria	774	7	2.5	408	6	ADP08173	Adp08173 Neisseria
702	7	2.5	348	7	ABO68187	Abu68187 Pseudomon	775	7	2.5	410	6	ABP78247	Abp78247 N. gonorr
703	7	2.5	349	6	ABU35385	Abu35385 Protein e	776	7	2.5	415	8	ADK48165	Adk48165 Streptoco
704	7	2.5	349	6	ABJ37500	Abj37500 HCV relat	777	7	2.5	416	8	ADJ56873	Adj56873 Corn TIG
705	7	2.5	350	6	ABJ37498	Abj37498 HCV relat	778	7	2.5	418	8	ADM94396	Adm94396 Soybean M
706	7	2.5	351	8	ADN19978	Adn19978 Bacterial	779	7	2.5	424	4	AAG90605	Aag90605 C glutami
707	7	2.5	352	6	ABU23954	Abu23954 Protein e	780	7	2.5	424	6	ABJ37501	Abj37501 HCV relat
708	7	2.5	352	8	ADN23486	Adn23486 Bacterial	781	7	2.5	424	8	ADS22111	Ads22111 Bacterial
709	7	2.5	353	6	ABJ26119	Abj26119 Aspergill	782	7	2.5	425	8	ADN20956	Adn20956 Bacterial
710	7	2.5	354	2	AAJ48405	Aay48405 Human pro	783	7	2.5	427	5	ABM47845	Abm47845 Listeria
711	7	2.5	354	8	ADN20147	Adn20147 Bacterial	784	7	2.5	427	6	ABU32710	Abu32710 Protein e
712	7	2.5	357	8	ADQ76692	Adq76692 Human KIM	785	7	2.5	429	6	ADR95180	Adr95180 Novel S.
713	7	2.5	358	2	AAR20715	Aar20715 C10-21 NA	786	7	2.5	431	6	ABU21312	Abu21312 Protein e
714	7	2.5	358	6	ABU49844	Abu49844 Protein e	787	7	2.5	433	6	ABU22103	Abu22103 Protein e
715	7	2.5	358	6	ABU24804	Abu24804 Protein e	788	7	2.5	435	8	ADN21346	Adn21346 Bacterial
716	7	2.5	359	6	ABR58582	Abu58582 Human can	789	7	2.5	443	4	ABU30887	Abu30887 Novel hum
717	7	2.5	359	6	ABP70439	Abp70439 Amino aci	790	7	2.5	445	4	ABB63068	Abb63068 Drosophil
718	7	2.5	359	6	ABP70441	Abp70441 Amino aci	791	7	2.5	445	8	ADG96700	Adg96700 Drosophil
719	7	2.5	359	6	ABP70438	Abp70438 Amino aci	792	7	2.5	447	4	ABG24991	Abg24991 Novel hum
720	7	2.5	359	6	ABR48174	Abu48174 Human bla	793	7	2.5	451	4	ABG16737	Abg16737 Novel hum
721	7	2.5	359	6	AAO26680	Aao26680 KIM-1 rel	794	7	2.5	452	6	ABU27650	Abu27650 Protein e
722	7	2.5	359	7	ADE36594	Ade36594 Human NOV	795	7	2.5	452	8	ADR27657	Adr27657 OB-RGRP L
723	7	2.5	359	8	ADN38984	Adn38984 Cancex/an	796	7	2.5	453	5	ADP27669	Adp27669 MYO47 LUC
724	7	2.5	359	8	ADQ76690	Adq76690 Human kid	797	7	2.5	453	5	ABP65641	Abp65641 Bifidobac
725	7	2.5	360	6	ABU25180	Abu25180 Protein e	798	7	2.5	456	8	ADS29239	Ads29239 Bacterial
726	7	2.5	361	3	AAJ32202	Aay32202 Human rec	799	7	2.5	460	8	ADS41814	Ads41814 Bacterial
727	7	2.5	361	4	AAJ93218	Aaj93218 Human pol	800	7	2.5	465	2	AAW31885	Aaw31885 HCV-1 non
728	7	2.5	361	4	AAE03646	Aae03646 Angiogene	801	7	2.5	465	8	ADQ76695	Adq76695 Mouse kim
729	7	2.5	361	6	ABR64256	Abu64256 Murine LA	802	7	2.5	473	5	AAW50076	Aaw50076 HCV NS3 h
730	7	2.5	361	7	ADO36769	Ado36769 Murine LA	803	7	2.5	489	6	ADO08674	Ado08674 Alloiococ
731	7	2.5	361	8	ADL30591	Adl30591 Human pro	804	7	2.5	490	7	ABO78464	Abu78464 Pseudomon
732	7	2.5	361	8	ADQ19404	Adq19404 Human sof	805	7	2.5	490	8	ADS43323	Ads43323 Bacterial
733	7	2.5	361	8	ABM80632	Abm80632 Tumour-as	806	7	2.5	491	4	ABM58307	Abm58307 Drosophil
734	7	2.5	364	6	ABP70443	Abp70443 Amino aci	807	7	2.5	491	4	ABM67058	Abm67058 Drosophil
735	7	2.5	364	6	ABP70442	Abp70442 Amino aci	808	7	2.5	491	7	ADK11397	Adk11397 Drosophil
736	7	2.5	364	6	ABJ37502	Abj37502 HCV relat	809	7	2.5	491	7	ADK11399	Adk11399 Drosophil
737	7	2.5	365	6	ABP70440	Abp70440 Amino aci	810	7	2.5	491	8	ADS96582	Ads96582 Drosophil
738	7	2.5	366	4	ABB61562	Abb61562 Drosophil	811	7	2.5	492	8	ADN20281	Adn20281 Bacterial
739	7	2.5	368	8	ADL35838	Adl35838 Human sin	812	7	2.5	493	8	ADS4658	Ads4658 Bacterial
740	7	2.5	368	8	ABM80095	Abm80095 Tumour-as	813	7	2.5	495	8	ADS30904	Ads30904 Bacterial
741	7	2.5	368	8	ADN25990	Adn25990 Bacterial	814	7	2.5	498	8	ADS28858	Ads28858 Bacterial
742	7	2.5	370	2	AAR29528	Aar29528 HCV antig	815	7	2.5	499	5	ABP26573	Abp26573 Streptoco
743	7	2.5	370	3	AAJ74818	Aay74818 Neisseria	816	7	2.5	504	5	ABP63086	Abp63086 FLO11 Gen
744	7	2.5	370	3	AAJ74819	Aay74819 Neisseria	817	7	2.5	505	7	ABO65745	Abu65745 Klebsiell
745	7	2.5	370	3	AAJ74820	Aay74820 Neisseria	818	7	2.5	513	4	AAB69032	Aab69032 HCV recom
746	7	2.5	370	6	ABU16755	Abu16755 Protein e	819	7	2.5	513	5	ABP30089	Abp30089 Streptoco
747	7	2.5	370	8	ADO80311	Ado80311 M. catarr	820	7	2.5	513	6	ABU01157	Abu01157 S. pneumo
748	7	2.5	370	8	ADO80311	Ado80311 Xylella s	821	7	2.5	513	6	ABP81364	Abp81364 Streptoco
749	7	2.5	370	8	ADO80309	Ado80309 Xylella s	822	7	2.5	513	7	ABW01897	Abw01897 HCV CKS-3
750	7	2.5	371	8	ADN26872	Adn26872 Bacterial	823	7	2.5	513	8	ADK46256	Adk46256 Streptoco
751	7	2.5	371	8	ADN26874	Adn26874 Bacterial	824	7	2.5	513	8	ADS42400	Ads42400 Bacterial
752	7	2.5	372	2	AAW56626	Aaw56626 Staphyloc	825	7	2.5	518	6	ABM70162	Abm70162 Photornab
753	7	2.5	372	6	ADA34389	Ada34389 Acinetoba	826	7	2.5	518	8	ADQ76691	Adq76691 Human KIM
754	7	2.5	374	7	ADI23989	Adi23989 Construct	827	7	2.5	519	8	ADS41654	Ads41654 Bacterial
755	7	2.5	377	6	ABJ18505	Abj18505 Human Cry	828	7	2.5	521	4	AAB78945	Aab78945 C. glutam

829	7	2.5	522	3	AAG49803	Aag49803 Arabidops	902	7	2.5	582	8	ADS42666	Ads42666 Bacterial
830	7	2.5	522	8	ADN5829	Adn25829 Bacterial	903	7	2.5	582	8	ADN18131	Adn18131 Bacterial
831	7	2.5	524	5	AAE13099	Aae13099 Staphyloc	904	7	2.5	583	8	ADS42479	Ads42479 Bacterial
832	7	2.5	524	8	ADS45022	Ads45022 Staphyloc	905	7	2.5	585	2	NAR58589	Nar58589 Hepatitis
833	7	2.5	526	4	ABG28548	Abg28548 Novel hum	906	7	2.5	585	4	ABG24297	Abg24297 Novel hum
834	7	2.5	528	6	ABM69162	Abm69162 Photorhab	907	7	2.5	585	6	AAE37951	Aae37951 Pseudomon
835	7	2.5	528	8	ADH44162	Adh44162 Hepatitis	908	7	2.5	585	8	ADL17780	Adl17780 Hepatitis
836	7	2.5	528	8	ADN37289	Adn37289 Barley st	909	7	2.5	585	8	ADS23862	Ads23862 Bacterial
837	7	2.5	529	7	ADB70185	Adb70185 C. neofor	910	7	2.5	587	4	AAU35367	Aau35367 Haemophil
838	7	2.5	529	8	ADS21119	Ads21119 Bacterial	911	7	2.5	587	4	AAB88504	Aab88504 Haemophil
839	7	2.5	530	6	ABU21280	Abu21280 Protein e	912	7	2.5	587	5	AAU91435	Aau91435 Haemophil
840	7	2.5	530	6	ABU22304	Abu22304 Protein e	913	7	2.5	589	6	ABU30139	Abu30139 Protein e
841	7	2.5	533	4	AAU35783	Aau35783 Helicobac	914	7	2.5	589	8	ADS29831	Ads29831 Bacterial
842	7	2.5	533	6	ABU30893	Abu30893 Protein e	915	7	2.5	590	6	ABM70726	Abm70726 Photorhab
843	7	2.5	537	8	ADS22392	Ads22392 Bacterial	916	7	2.5	590	8	ADN18082	Adn18082 Bacterial
844	7	2.5	539	8	ADN25209	Adn25209 Bacterial	917	7	2.5	591	8	ADF70703	Adf70703 Acetic-ac
845	7	2.5	545	6	ABU23013	Abu23013 Protein e	918	7	2.5	592	8	ADN25035	Adn25035 Bacterial
846	7	2.5	546	7	ADC94354	Adc94354 E. faeciu	919	7	2.5	593	7	ADF05083	Adf05083 Bacterial
847	7	2.5	547	4	AAB79015	Aab79015 C. glutam	920	7	2.5	593	8	ADN20003	Adn20003 Bacterial
848	7	2.5	547	4	AAG90928	Aag90928 C. glutam	921	7	2.5	594	4	AAU57050	Aau57050 Propionib
849	7	2.5	547	7	ABR63524	Abf63524 C. glutam	922	7	2.5	594	6	ABM53569	Abm53569 Propionib
850	7	2.5	547	7	ADL65547	Adl65547 C. glutam	923	7	2.5	594	6	ABM73376	Abm73376 Staphyloc
851	7	2.5	548	7	ADC97000	Adc97000 E. faeciu	924	7	2.5	594	7	ADC97623	Adc97623 E. faeciu
852	7	2.5	549	7	ADC73281	Adc73281 Escherich	925	7	2.5	595	7	ABG75195	Abg75195 M. licheni
853	7	2.5	549	8	ADS25614	Ads25614 Bacterial	926	7	2.5	598	4	AAU65295	Aau65295 Propionib
854	7	2.5	554	2	AAW50077	Aar50077 NANBH vir	927	7	2.5	598	5	ABB92998	Abb92998 Herbicida
855	7	2.5	554	2	AAW48661	Aaw48661 RG fusion	928	7	2.5	598	6	ABM61814	Abm61814 Propionib
856	7	2.5	554	4	AAG90339	Aag90339 C. glutam	929	7	2.5	598	8	ADN22808	Adn22808 Bacterial
857	7	2.5	554	8	ADJ81682	Adj81682 Non-A-non	930	7	2.5	599	8	ADS28276	Adn28276 Bacterial
858	7	2.5	554	8	ADM94400	Adm94400 Soybean M	931	7	2.5	601	8	ADN22277	Adn22277 Bacterial
859	7	2.5	555	6	ABU19827	Abu19827 Protein e	932	7	2.5	602	6	ABU23460	Abu23460 Protein e
860	7	2.5	555	7	ADC73279	Adc73279 Escherich	933	7	2.5	604	5	ABBA48305	Abb48305 Listeria
861	7	2.5	556	8	ADS29774	Ads29774 Bacterial	934	7	2.5	607	5	ABP62771	Abp62771 Protein f
862	7	2.5	558	2	AAW48662	Aaw48662 GR fusion	935	7	2.5	607	6	ABP58190	Abp58190 Luciferas
863	7	2.5	558	4	ABG06559	Abg06559 Novel hum	936	7	2.5	607	7	ADJ72182	Adj72182 Streptomy
864	7	2.5	558	5	ABP27849	Abp27849 Streptoco	937	7	2.5	608	8	ADF70705	Adf70705 Acetic-ac
865	7	2.5	559	6	ABU21221	Abu21221 Protein e	938	7	2.5	609	2	AAR51170	Aar51170 Hepatitis
866	7	2.5	560	6	ABU00845	Abu00845 S. pneumo	939	7	2.5	612	8	ADS29013	Ads29013 Bacterial
867	7	2.5	560	6	ABP81330	Abp81330 Streptoco	940	7	2.5	613	4	AAU04887	Aau04887 Micromono
868	7	2.5	560	8	ADS30310	Ads30310 Bacterial	941	7	2.5	613	5	AAE19893	Aae19893 Hepatitis
869	7	2.5	564	6	ABU40586	Abu40586 Protein e	942	7	2.5	613	6	ABU28306	Abu28306 Protein e
870	7	2.5	566	8	ADH39713	Adh39713 Streptomy	943	7	2.5	613	7	ABW00344	Abw00344 Hepatitis
871	7	2.5	568	5	ABP27905	Abp27905 Streptoco	944	7	2.5	613	8	ADS23090	Ads23090 Bacterial
872	7	2.5	568	6	ABU46439	Abu46439 Protein e	945	7	2.5	614	6	ABM66127	Abm66127 Propionib
873	7	2.5	570	6	ABM72766	Abm72766 Staphyloc	946	7	2.5	615	2	AAW37807	Aaw37807 Nonstruct
874	7	2.5	571	6	ABU49048	Abu49048 Protein e	947	7	2.5	621	6	ABU20490	Abu20490 Protein e
875	7	2.5	572	8	ADS26086	Ads26086 Bacterial	948	7	2.5	621	8	ADS21702	Ads21702 Bacterial
876	7	2.5	573	5	ABP28687	Abp28687 Streptoco	949	7	2.5	623	7	ABO82427	Abo82427 Pseudomon
877	7	2.5	573	5	ABH48813	Abh48813 Listeria	950	7	2.5	623	6	ADB09723	Adb09723 Alloiooc
878	7	2.5	574	6	ADB11648	Adb11648 Alloiooc	951	7	2.5	625	8	ADS23228	Ads23228 Bacterial
879	7	2.5	575	4	ABB47263	Abb47263 Enterococ	952	7	2.5	625	6	ADN23228	Adn23228 Bacterial
880	7	2.5	575	6	ABU11393	Abu11393 Protein e	953	7	2.5	628	2	AAW85701	Aaw85701 Pinene sy
881	7	2.5	575	6	ABM72335	Abm72335 Staphyloc	954	7	2.5	628	3	AAI90837	Aai90837 Grand fir
882	7	2.5	575	7	ADH87501	Adh87501 Enterococ	955	7	2.5	628	4	AAW69371	Aaw69371 Grand fir
883	7	2.5	577	8	ADN20264	Adn20264 Bacterial	956	7	2.5	630	2	ADN33110	Adn33110 Hepatitis
884	7	2.5	577	8	ADN20361	Adn20361 Bacterial	957	7	2.5	631	2	AAW82854	Aaw82854 NS3 serin
885	7	2.5	579	8	ADS21357	Ads21357 Bacterial	958	7	2.5	631	2	AAW31884	Aaw31884 A nonstru
886	7	2.5	580	5	ABP40766	Abp40766 Staphyloc	959	7	2.5	631	2	AAW26160	Aaw26160 Serine pr
887	7	2.5	580	8	ADS08083	Ads08083 Staphyloc	960	7	2.5	631	2	AAW93482	Aaw93482 HCV NS3 p
888	7	2.5	581	8	ADS30307	Ads30307 Bacterial	961	7	2.5	631	2	AAW14354	Aaw14354 Hepatitis
889	7	2.5	581	8	ADN17801	Adn17801 Bacterial	962	7	2.5	631	2	AAW15806	Aaw15806 HCV strai
890	7	2.5	581	8	ADN27071	Adn27071 Bacterial	963	7	2.5	631	3	AAW41972	Aaw41972 Human ORF
891	7	2.5	582	4	AAU38413	Aau38413 Salmonell	964	7	2.5	631	3	AAW18158	Aaw18158 Hepatitis
892	7	2.5	582	4	AAU34522	Aau34522 E. coli c	965	7	2.5	632	5	AAE21847	Aae21847 Hepatitis
893	7	2.5	582	6	ABU49428	Abu49428 Protein e	966	7	2.5	632	5	AAE19905	Aae19905 Hepatitis
894	7	2.5	582	6	ABU48048	Abu48048 Protein e	967	7	2.5	632	6	ABU23866	Abu23866 Protein e
895	7	2.5	582	6	ABU31837	Abu31837 Protein e	968	7	2.5	632	7	ABW00356	Abw00356 Hepatitis
896	7	2.5	582	6	ABU45164	Abu45164 Protein e	969	7	2.5	632	8	ADG47669	Adg47669 HCV NS3/4
897	7	2.5	582	6	ABU50086	Abu50086 Protein e	970	7	2.5	632	8	ADO36213	Ado36213 Hepatitis
898	7	2.5	582	6	ABU47313	Abu47313 Protein e	971	7	2.5	632	8	ADO79387	Ado79387 Hepatitis
899	7	2.5	582	6	ABU28578	Abu28578 Protein e	972	7	2.5	633	3	AAW81755	Aaw81755 Streptoco
900	7	2.5	582	6	ABU39189	Abu39189 Protein e	973	7	2.5	633	4	AAU37725	Aau37725 Streptoco
901	7	2.5	582	7	ABO65563	AbO65563 Klebsiell	974	7	2.5	633	4	AAU37725	Aau37725 Streptoco

Adn25829	Bacterial
Aae13099	Staphyloc
Ads45022	Staphyloc
Abg28548	Novel hum
Abm69162	Photorhab
Adh44162	Hepatitis
Adn37289	Barley st
Adb70185	C. neofor
Ads21119	Bacterial
Abu21280	Protein e
Abu22304	Protein e
Aau35783	Helicobac
Abu30893	Protein e
Adn22392	Bacterial
Adn25209	Bacterial
Abu23013	Protein e
Adc94354	E. faeciu
Aab79015	C. glutam
Aag90928	C. glutam
Abf63524	C. glutam
Adl65547	C. glutam
Adc97000	E. faeciu
Adc73281	Escherich
Ads25614	Bacterial
Aar50077	NANBH vir
Aaw48661	RG fusion
Aag90339	C. glutam
Adj81682	Non-A-non
Adm94400	Soybean M
Abu19827	Protein e
Adc73279	Escherich
Ads29774	Bacterial
Aaw48662	GR fusion
Abg06559	Novel hum
Abp27849	Streptoco
Abu21221	Protein e
Abu00845	S. pneumo
Abp81330	Streptoco
Ads30310	Bacterial
Abu40586	Protein e
Adh39713	Streptomy
Abp27905	Streptoco
Abu46439	Protein e
Abm72766	Staphyloc
Abu49048	Protein e
Ads26086	Bacterial
Abp28687	Streptoco
Abh48813	Listeria
Adb11648	Alloiooc
Abb47263	Enterococ
Abu11393	Protein e
Abm72335	Staphyloc
Adh87501	Enterococ
Adn20264	Bacterial
Adn20361	Bacterial
Ads21357	Bacterial
Abp40766	Staphyloc
Ads08083	Staphyloc
Ads30307	Bacterial
Adn17801	Bacterial
Adn27071	Bacterial
Aau38413	Salmonell
Aau34522	E. coli c
Abu49428	Protein e
Abu48048	Protein e
Abu31837	Protein e
Abu45164	Protein e
Abu50086	Protein e
Abu47313	Protein e
Abu28578	Protein e
Abu39189	Protein e
AbO65563	Klebsiell

975 7 2.5 633 6 ABU01533 S. pneumo
976 7 2.5 633 6 ABU46048 Protein e
977 7 2.5 633 8 ADK47288 Streptoco
978 7 2.5 634 6 ADB09721 Allolococ
979 7 2.5 635 5 ABP27552 Streptoco
980 7 2.5 635 5 ABB54378 Lactococ
981 7 2.5 635 6 ABU46609 Protein e
982 7 2.5 635 6 ABR42556 Novobioc
983 7 2.5 635 8 ADS29366 Bacteri
984 7 2.5 636 5 ABP30300 Streptoco
985 7 2.5 636 6 ABU41603 Protein e
986 7 2.5 637 6 ABM69282 Photorhab
987 7 2.5 637 6 ABU44131 Protein e
988 7 2.5 638 4 AAE10068 Hepatitis
989 7 2.5 639 6 ABU49363 Protein e
990 7 2.5 642 6 ABU24552 Protein e
991 7 2.5 644 5 ABP27551 Streptoco
992 7 2.5 645 6 ABU21789 Protein e
993 7 2.5 645 8 ADS23263 Bacteri
994 7 2.5 646 2 AAY17894 HCV NS4A-
995 7 2.5 646 2 AAY17892 HCV NS4A-
996 7 2.5 646 2 AAY24950 HCV NS4A-
997 7 2.5 647 8 Adn22057 Bacteri
998 7 2.5 647 8 Adn24816 Bacteri
999 7 2.5 649 2 AAR14546 hSOD-HCV
1000 7 2.5 649 6 ABU19934 Protein e

ALIGNMENTS

RESULT 1
AAY81709
ID AAY81709 standard; protein; 279 AA.
XX AAY81709;
DT 02-JUN-2000 (first entry)
XX Streptococcus pneumoniae protein sequence ID2.
XX Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS;
KW bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism;
KW kidney disease; diabetes; immunosuppressive disorder; otitis media;
KW pneumococcal septicaemia; sinusitis; meningitis; therapy.
XX Streptococcus pneumoniae.
XX WO200006738-A2.
XX 10-FEB-2000.
XX 27-JUL-1999; 99WO-GB002452.
XX 27-JUL-1998; 98GB-00016336.
XX 19-MAR-1999; 99US-0125329P.
XX (MICR-) MICROBIAL TECHNIQS LTD.
XX Le Page RWF, Wells JM, Hanniffy SB, Hanebro PM;
XX WPI; 2000-195301/17.
XX N-PSDB; AAZ91805.
XX Streptococcal proteins and polynucleotides useful for diagnosis,
XX treatment and prophylaxis of bacterial infections.
XX Claim 2; Page 40; 76pp; English.
XX This sequence represents a Streptococcus pneumoniae protein of the
CC invention. The proteins (or their homologues, derivatives and/or
CC fragments) are useful as immunogens or antigens. Immunogenic or antigenic
CC compositions comprising the proteins are useful as vaccines and also in

CC diagnostic assays. The sequences are useful for the detection or
CC diagnosis of S. pneumoniae infection, by contacting a sample to be tested
CC with them. Agents capable of antagonising, inhibiting or interfering with
CC the function or expression of the protein or polypeptide are useful in
CC medical compositions in the treatment or prophylaxis of S. pneumoniae
CC infection. As the sequences can be used to treat S. pneumoniae infection,
CC they can be used to treat bacterial pneumonia, which has high rates in
CC young children, the elderly, and in patients with predisposing conditions
CC such as asplenia, heart, lung and kidney disease, diabetes, alcoholism,
CC or with immunosuppressive disorders, especially AIDS. They can also be
CC used to treat pneumococcal septicaemia, otitis media, sinusitis, and
CC meningitis
XX
SQ Sequence 279 AA;
Query Match 100.0%; Score 279; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 7.7e-263;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIALENVNTTQEGTPTLASAALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLLVPS 60
DB 1 MGIALENVNTTQEGTPTLASAALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLLVPS 60
QY 61 QGSVRVFDLTITSTSKNKDIQIRKQVGLVFOFAENQIPEETVLKDVAFGPQFVGVSEED 120
DB 61 QGSVRVFDLTITSTSKNKDIQIRKQVGLVFOFAENQIPEETVLKDVAFGPQFVGVSEED 120
QY 121 AVKTAREKALVGIDESLFDSPFELSGQGMRRVAJAGILAMEPAILVLDEPTAGLDPLG 180
DB 121 AVKTAREKALVGIDESLFDSPFELSGQGMRRVAJAGILAMEPAILVLDEPTAGLDPLG 180
QY 181 RKELMTLPFKLHQSGMTIVLVTHLMDDDVAEYANQVYVMEKGLVKGKPSDVQDVVFME 240
DB 181 RKELMTLPFKLHQSGMTIVLVTHLMDDDVAEYANQVYVMEKGLVKGKPSDVQDVVFME 240
QY 241 EVQLGVPKITAFCKRLADRGVSPFKRLPIKIEEFKESLNG 279
DB 241 EVQLGVPKITAFCKRLADRGVSPFKRLPIKIEEFKESLNG 279
RESULT 2
ABU02751
ID ABU02751 standard; protein; 279 AA.
XX ABU02751;
AC ABU02751;
DT 23-OCT-2003 (revised)
DT 11-FEB-2003 (first entry)
XX S. pneumoniae type 4 strain protein from coding region #2330.
XX Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
KW antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
KW gene therapy; vaccine.
XX Streptococcus pneumoniae; type 4 strain.
OS WO200277021-A2.
XX 03-OCT-2002.
XX 27-MAR-2002; 2002WO-IB002163.
XX 27-MAR-2001; 2001GB-00007658.
XX (CHIR-) CHIRON SPA.
XX (GENO-) INST GENOMIC RES.
XX Masignani V, Tettelin H, Fraser C;
XX WPI; 2003-040579/03.
XX N-PSDB; ABX08042.

QY	241	EVOLGVPKITAFCCKRLADRGVSFKRLP	267	Db	181	RKELMTLTKKLLHSGMTIVLTHLMDVAEYANQVYVMEKGRIVKGGKPSDFQDVVFME	240
Db	241	EVOLGVPKITAFCCKRLADRGVSFKRLP	267	QY	241	EVOLGVPKITAFCCKRLADRGVSFKRLP	267
Db	241	EVOLGVPKITAFCCKRLADRGVSFKRLP	267	Db	241	EVOLGVPKITAFCCKRLADRGVSFKRLP	267
RESULT 4							
ADK47865							
ID	ADK47865	standard; protein; 279 AA.					
XX	AC	ADK47865;					
XX	DT	20-MAY-2004 (first entry)					
XX	DE	Streptococcus pneumoniae protein, Seq ID No 4380.					
XX	KW	Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.					
XX	OS	Streptococcus pneumoniae.					
XX	PN	US6699703-B1.					
XX	PD	02-MAR-2004.					
XX	PF	26-MAY-2000; 2000US-00583110.					
XX	PR	02-JUL-1997; 97US-0051553P.					
XX	PR	12-MAY-1998; 98US-0085131P.					
XX	PR	30-JUN-1998; 98US-00107433.					
XX	PA	(GENO-) GENOME THERAPEUTICS CORP.					
XX	PI	Doucette-Stamm L, Bush D, Zeng Q, Opperman T, Houseweart CE;					
XX	PI	WPI; 2004-212399/20.					
XX	DR	N-PSDB; ADK45204.					
XX	PT	New nucleic acid molecules and polypeptides useful for diagnosing,					
XX	PT	preventing and treating pathological conditions resulting from bacterial					
XX	PT	infection, e.g. Streptococcus pneumoniae infection, and in drug					
XX	PT	screening.					
XX	PS	Disclosure; SEQ ID NO 4380; 301pp; English.					
XX	CC	The invention relates to isolated Streptococcus pneumoniae nucleic acids					
XX	CC	and polypeptides. The nucleic acids and proteins are useful for					
XX	CC	diagnosing, preventing and treating pathological conditions resulting					
XX	CC	from bacterial infection, such as S. pneumoniae infection. These may also					
XX	CC	be used for drug screening procedures. The present sequence represents a					
XX	CC	Streptococcus pneumoniae polypeptide of the invention. Note: The sequence					
XX	CC	data for this patent did not appear in the printed specification but was					
XX	CC	obtained in electronic format directly from USPTO at					
XX	CC	seqdata.uspto.gov/sequence.html.					
XX	QY	Sequence 279 AA;					
XX	QY	Query Match 95.7%; Score 267; DB 8; Length 279;					
XX	QY	Best Local Similarity 100.0%; Pred. No. 3.7e-251;					
XX	QY	Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MGTALENVNTYQGTPLASAAISDVSLTIEDSGSYTALIGHTSGKSTILQLLGLLVPS	60	QY	1	MGTALENVNTYQGTPLASAAISDVSLTIEDSGSYTALIGHTSGKSTILQLLGLLVPS	60
Db	1	MGTALENVNTYQGTPLASAAISDVSLTIEDSGSYTALIGHTSGKSTILQLLGLLVPS	60	Db	1	MGTALENVNTYQGTPLASAAISDVSLTIEDSGSYTALIGHTSGKSTILQLLGLLVPS	60
QY	61	QGSVRVFDTLITSTSKNKRQIRKQVGLVQFAENQIFETVLKDVAFQPNFGVSEED	120	QY	61	QGSVRVFDTLITSTSKNKRQIRKQVGLVQFAENQIFETVLKDVAFQPNFGVSEED	120
Db	61	QGSVRVFDTLITSTSKNKRQIRKQVGLVQFAENQIFETVLKDVAFQPNFGVSEED	120	Db	61	QGSVRVFDTLITSTSKNKRQIRKQVGLVQFAENQIFETVLKDVAFQPNFGVSEED	120
QY	121	AVKTAREKIALVGI DESLFRSPPELGGQRRVAIAGILAMEPAIILVDEPTAGLDPLG	180	QY	121	AVKTAREKIALVGI DESLFRSPPELGGQRRVAIAGILAMEPAIILVDEPTAGLDPLG	180
Db	121	AVKTAREKIALVGI DESLFRSPPELGGQRRVAIAGILAMEPAIILVDEPTAGLDPLG	180	Db	121	AVKTAREKIALVGI DESLFRSPPELGGQRRVAIAGILAMEPAIILVDEPTAGLDPLG	180
QY	181	RKELMTLTKKLLHSGMTIVLTHLMDVAEYANQVYVMEKGRIVKGGKPSDFQDVVFME	240	QY	181	RKELMTLTKKLLHSGMTIVLTHLMDVAEYANQVYVMEKGRIVKGGKPSDFQDVVFME	240
Db	181	RKELMTLTKKLLHSGMTIVLTHLMDVAEYANQVYVMEKGRIVKGGKPSDFQDVVFME	240	Db	181	RKELMTLTKKLLHSGMTIVLTHLMDVAEYANQVYVMEKGRIVKGGKPSDFQDVVFME	240

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QY 1 MGTALENNVETYOEGTPLASAAALSDVSLTIEDGSGYTTALIGHTGSGKSTILQLLNGLLVPS 60
DB 2 MGTALENNVETYOEGTPLASAAALSDVSLTIEDGSGYTTALIGHTGSGKSTILQLLNGLLVPS 61
QY 61 QGSRVRFDTLITSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
DB 62 QGSRVRFDTLITSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 121
QY 121 AVKTAREKALVGLIDESLFDSPSPPELGGQMRRAIAGILAMEPAILVLDDEPTAGLDPLG 180
DB 122 AVKTAREKALVGLIDESLFDSPSPPELGGQMRRAIAGILAMEPAILVLDDEPTAGLDPLG 181
QY 181 RKELMTLFPKLLHOSGMTIVLVTMLDMDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFME 240
DB 182 RKELMTLFPKLLHOSGMTIVLVTMLDMDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFME 241
QY 241 EVQLGVPKITAFCKRLADRGVSFKRLP 267
DB 242 EVQLGVPKITAFCKRLADRGVSFKRLP 268

RESULT 6
AAU37847
ID AAU37847 standard; protein; 279 AA.
XX
AC AAU37847;
XX
DT 14-FEB-2002 (first entry)
XX
DE Streptococcus pneumoniae cellular proliferation protein #276.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
OS Streptococcus pneumoniae.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
XX
DR N-PSDB; AAS55706.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX
XX Example 3; SEQ ID NO 13440; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX proteins used in proliferation, to express these proteins, and to obtain
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CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 279 AA;
XX
Query Match 59.9%; Score 167; DB 4; Length 279;
Best Local Similarity 99.6%; Pred. No. 9e-154;
Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 YQSGTPLASAAALSDVSLTIEDGSGYTTALIGHTGSGKSTILQLLNGLLVPSQGSVRVFTLI 71
DB 12 YQSGTPLASAAALSDVSLTIEDGSGYTTALIGHTGSGKSTILQLLNGLLVPSQGSVRVFTLI 71
QY 72 TSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEEDAVKTAREKAL 131
DB 72 TSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEEDAVKTAREKAL 131
QY 132 VGIDESLFDSPPELGGQMRRAIAGILAMEPAILVLDDEPTAGLDPLGRKELMTLFPKL 191
DB 132 VGIDESLFDSPPELGGQMRRAIAGILAMEPAILVLDDEPTAGLDPLGRKELMTLFPKL 191
QY 192 HQSGMTIVLVTMLDMDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFMEVQLGVPKITA 251
DB 192 HQSGMTIVLVTMLDMDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFMEVQLGVPKITA 251
QY 252 FCRLADRGVSFKRLPIKIEEFKESLNG 279
DB 252 FCRLADRGVSFKRLPIKIEEFKESLNG 279

RESULT 7
ABU46314
ID ABU46314 standard; protein; 279 AA.
XX
AC ABU46314;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #31841.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Streptococcus pneumoniae.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX
XX N-PSDB; ACA50184.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
```


PT isolate candidate molecules for rational drug discovery programs.

XX
XX
PS Claim 25; SEQ ID NO 74238; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC the gene product; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 279 AA;

Query Match 59.9%; Score 167; DB 6; Length 279;
Best Local Similarity 99.6%; Pred. No. 9e-154;
Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 YQSGTPLASALSDVSLTIEDGYSYALIGHTGSGKSTILOLLNGLLVPSQSVRVPTLI 71
DB 12 YQSGTPLASALSDVSLTIEDGYSYALIGHTGSGKSTILOLLNGLLVPSQSVRVPTLI 71
QY 72 TSTSKNKDIIQIRKQGLVQFAENQIFETVLKDVAFQNFQVSEEDAVKTAREKIAL 131
DB 72 TSTSKNKDIIQIRKQGLVQFAENQIFETVLKDVAFQNFQVSEEDAVKTAREKIAL 131
QY 132 VGIDESLFDSPPELSCGQMRRAIAGILAMEPAILVLDEPTAGLDPLGRKELMTLPKKL 191
DB 132 VGIDESLFDSPPELSCGQMRRAIAGILAMEPAILVLDEPTAGLDPLGRKELMTLPKKL 191
QY 192 HQSGMTIVLTHLMDDVAEYANQVYVMEKGRVKGKPSDFQDVPMEEVQLGVPKITA 251
DB 192 HQSGMTIVLTHLMDDVAEYANQVYVMEKGRVKGKPSDFQDVPMEEVQLGVPKITA 251
QY 252 FCRLADRGVSFKRLPIKIEFKESLNG 279
DB 252 FCRLADRGVSFKRLPIKIEFKESLNG 279

RESULT 8
ABB53584
ID ABB53584 standard; protein; 288 AA.

XX
AC ABB53584;
XX
XX 29-AUG-2003 (revised)
DT 16-MAY-2002 (first entry)
XX
XX Lactococcus lactis protein ychE.

XX
KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
XX
OS Lactococcus lactis; IL1403.
PN
PN PR2807446-A1.
XX
PD 12-OCT-2001.
XX
PF 11-APR-2000; 2000FR-00004630.
XX
PR 11-APR-2000; 2000FR-00004630.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
XX
XX WPI; 2002-043418/06.
XX
XX New nucleotide sequence useful in the identification of Lactococcus
XX lactis and related species.
XX
PS Claim 6; SEQ ID NO 286; 2504pp; French.

XX
CC The present invention is related to a Lactococcus lactis nucleotide
CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic
CC acid sequence is useful in the detection and/or amplification of nucleic
CC acid sequence, particularly to identify Lactococcus lactis or related
CC species. The proteins of the invention are useful for the biosynthesis or
CC biodegradation of a composition of interest. The invention helps research
CC in lactic bacteria, particularly useful in the production of yogurt and
CC cheese. Note: The sequence data for this patent is based on equivalent
CC patent WO200177334 (published 18-OCT-2001) which is available in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to
XX
XX standardise OS field)
XX
SQ Sequence 288 AA;

Query Match 8.2%; Score 23; DB 5; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 142 SPFELSGQMRRAIAGILAMEP 164
DB 141 SPFELSGQMRRAIAGILAMEP 163

RESULT 9
ADK99877
ID ADK99877 standard; protein; 279 AA.
XX
XX AC ADK99877;
XX
DT 20-MAY-2004 (first entry)
XX
XX Streptococcus agalactiae ORF SAG2150-related protein 3.
DE immunogenic composition; group B Streptococcus; GBS; antibacterial;
KW streptococcal infection; vaccine; SAG.
XX
XX Streptococcus agalactiae.
XX
XX WO2004018646-A2.
XX
XX 04-MAR-2004.
XX
XX 26-AUG-2003; 2003WO-US026827.
XX
XX 26-AUG-2002; 2002US-0406237P.
PR 27-AUG-2002; 2002US-0406676P.
XX
XX 28-AUG-2002; 2002US-0406757P.

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OM protein - protein search, using sw model

Run on: October 28, 2005, 17:09:46 ; Search time 174 Seconds
(without alignments)
821.092 Million cell updates/sec

Title: US-09-769-744d-26

Perfect score: 1387

Sequence: 1 MGIALENNFTYQEGTPLAS.....GVSPKRLPIKIEPKESLNG 279

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1387	100.0	279	Q97N51	Q97N51 streptococ
2	1378	99.4	279	Q8DMY0	Q8DMY0 streptococ
3	1002.5	72.3	280	Q8DRS0	Q8DRS0 streptococ
4	971	70.0	280	Q99X12	Q99X12 streptococ
5	971	70.0	280	Q7CMM8	Q7CMM8 streptococ
6	969	69.9	280	Q8KSH2	Q8KSH2 streptococ
7	948	68.3	280	Q8DWR4	Q8DWR4 streptococ
8	948	68.3	280	Q8E2L3	Q8E2L3 streptococ
9	899.5	64.9	288	Q9CIS8	Q9CIS8 lactococcc
10	850.5	61.3	291	Q839D4	Q839D4 enterococ
11	849.5	61.2	295	Q88XV1	Q88XV1 lactobacill
12	729	52.6	276	Q70970	Q70970 bacillus su
13	727	52.4	289	Q65P76	Q65P76 bacillus li
14	710.5	51.2	286	Q8R7Y5	Q8R7Y5 thermoaer
15	704	50.8	289	Q74L61	Q74L61 lactobacill
16	700	50.5	293	Q81VQ1	Q81VQ1 bacillus th
17	700	50.5	293	Q81VQ1	Q81VQ1 bacillus th
18	699.5	50.4	289	Q8ETV6	Q8ETV6 oceanobacil
19	699	50.4	293	Q63H61	Q63H61 bacillus ce
20	699	50.4	293	Q73F66	Q73F66 bacillus ce
21	696.5	50.2	288	Q927N9	Q927N9 listeria in
22	695	50.1	293	Q81J15	Q81J15 bacillus ce
23	693.5	50.0	288	Q71WH8	Q71WH8 listeria mo
24	692.5	49.9	288	Q8Y455	Q8Y455 listeria mo
25	683	49.2	286	Q97EK9	Q97EK9 clostridium
26	679	49.0	288	Q890R3	Q890R3 clostridium
27	678	48.9	285	Q8XHV3	Q8XHV3 clostridium
28	658	47.4	288	Q67JX4	Q67JX4 symbiobacte
29	637.5	46.0	282	Q9KGD6	Q9KGD6 bacillus ha
30	634.5	45.7	308	Q6KHL2	Q6KHL2 mycoplasma
31	609	43.9	286	Q8CRI7	Q8CRI7 staphylococ

32 601.5 43.4 303 2 Q6MSQ2
33 601 43.3 305 2 Q6XYZ3
34 595.5 42.9 304 2 Q98QH4
35 592.5 42.7 286 2 Q6GELA
36 589.5 42.5 286 2 Q99S48
37 589.5 42.5 286 2 Q7A088
38 589.5 42.5 286 2 Q7A471
39 589.5 42.5 286 2 Q6G7A0
40 587.5 42.4 315 2 Q6F1W4
41 575 41.5 177 2 Q8VNL8
42 545 39.3 293 2 Q8R7Y4
43 540.5 39.0 304 1 Y180_MYCGE
44 533.5 38.5 303 1 Y180_MYCPN
45 517.5 37.3 318 2 Q7NAQ7

ALIGNMENTS

RESULT 1

Q97N51 PRELIMINARY; PRT; 279 AA.
AC Q97N51;
DT 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DE ABC transporter, ATP-binding protein.
GN OrderedLocusNames=SP2220;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T.,
RA Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus pneumoniae";
Science 293:498-506(2001).
RL -I- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AB007509; AAK76268.1; -.
DR HSP; P02915; 1B0U.
DR TIGR; SP2220; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 279 AA; 30525 MW; E051E473D082AD32 CRC64;

Query Match 100.0%; Score 1387; DB 2; Length 279;

Best Local Similarity 100.0%; Pred. No. 6.6e-88;

Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIALENNFTYQEGTPLASALSDVSLTIEDGSGYTLIGHTSGKSTIQLNGLLVPS 60
|||||

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Db      1 MGIALENVNFYQEGTPLASAAALSDVSLTIEDGSYALIGHTGSGKSTILQLLGLLVP 60
Qy      61 QGSVRVFTLTITSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGQNFQGVSEED 120
Db      61 QGSVRVFTLTITSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGQNFQGVSEED 120
Qy      121 AVKTAREKALVIGIDESLFDSPFELSGQWRRVAIAGILAMEPAILVLDSPTAGLDPLG 180
Db      121 AVKTAREKALVIGIDESLFDSPFELSGQWRRVAIAGILAMEPAILVLDSPTAGLDPLG 180
Qy      181 RKELMTLTKLHQSOGMTIVLVTHLMDVDAEYANQVYVMEKGRVKGKPSDVFDQVWVME 240
Db      181 RKELMTLTKLHQSOGMTIVLVTHLMDVDAEYANQVYVMEKGRVKGKPSDVFDQVWVME 240
Qy      241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
Db      241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279

RESULT 2
Q8DMY0 PRELIMINARY; PRT; 279 AA.
AC Q8DMY0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein ABC-NBP.
GN Name=ABC-NBP; OrderedLocNames=spr2025;
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=171101;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
RX DOI=10.1128/JB.183.19.5709-5717.2001;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Niclas T.I.,
RA Norris P.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE008566; AAL00827.1; -.
DR FIR; F98124; F98124.
DR HSP; P02915; I800.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 279 AA; 30553 MW; FB5A148C367A6032 CRC64;

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Query Match      99.3%; Score 1378; DB 2; Length 279;
Best Local Similarity 99.3%; Pred. No. 2.7e-87;
Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MGIALENVNFYQEGTPLASAAALSDVSLTIEDGSYALIGHTGSGKSTILQLLGLLVP 60
Db      1 MGIALENVNFYQEGTPLASAAALSDVSLTIEDGSYALIGHTGSGKSTILQLLGLLVP 60

```

```

Qy      61 QGSVRVFTLTITSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGQNFQGVSEED 120
Db      61 QGSVRVFTLTITSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGQNFQGVSEED 120
Qy      121 AVKTAREKALVIGIDESLFDSPFELSGQWRRVAIAGILAMEPAILVLDSPTAGLDPLG 180
Db      121 AVKTAREKALVIGIDESLFDSPFELSGQWRRVAIAGILAMEPAILVLDSPTAGLDPLG 180
Qy      181 RKELMTLTKLHQSOGMTIVLVTHLMDVDAEYANQVYVMEKGRVKGKPSDVFDQVWVME 240
Db      181 RKELMTLTKLHQSOGMTIVLVTHLMDVDAEYANQVYVMEKGRVKGKPSDVFDQVWVME 240
Qy      241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
Db      241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279

RESULT 3
Q8DRS0 PRELIMINARY; PRT; 280 AA.
AC Q8DRS0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative ABC transporter, ATP-binding protein; possible cobalt
DE transport system.
GN OrderedLocNames=SMU.2149c;
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=UAI59 / ATCC 700610 / Serotype c;
RX MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RX Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RX Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RX Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RX Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UAI59, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE015035; AAN59738.1; -.
DR HSP; P58101; I058.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30941 MW; 600ED3F5CC6F928A CRC64;

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Query Match      72.3%; Score 1002.5; DB 2; Length 280;
Best Local Similarity 70.0%; Pred. No. 2.3e-61;
Matches 196; Conservative 38; Mismatches 45; Indels 1; Gaps 1;

Qy      1 MGIALENVNFYQEGTPLASAAALSDVSLTIEDGSYALIGHTGSGKSTILQLLGLLVP 60
Db      1 MGIALENVNFYQEGTPLASAAALSDVSLTIEDGSYALIGHTGSGKSTILQLLGLLVP 60

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Qy      61 QGSVRVFTLTITSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGQNFQGVSEED 120
Db      61 EGTVLVDVAIRSDSKNKDIKIRKQVGLVFPQPESQLFDETVLKDVAFGQNFQGVSEED 120

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```
QY 121 AVKTAREKALVGDIDSLFDRSPFELSGGOMRRVAIAGILAMEPAIILVLDPTAGLDPLG 180
Db 121 ABKJAREKALVGIISSEELFEKPFELSGGOMRRVAIAGILAMEPSILVLDPTAGLDPLG 180
QY 181 RKELMTLFFKLHSGGMTIIVLTHLMDVVAIYANQVYVMEKGRVKGKPSDVFQDVVFME 240
Db 181 RRELMTLFFKLHSGGMTIIVLTHLMDVVAIYANQVYVMEKGRVKGKPSDVFQDVVFME 240
QY 241 EVOLGVPKITAFCKRLADRGVSFKLPIKIEEFKESL-NG 279
Db 241 SKQLGVPKITQFAAHLRERGITFDALPITLEBFVEAIKNG 280

RESULT 4
Q99X12 PRELIMINARY; PRT; 280 AA.
AC Q99X12;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Putative ABC transporter (ATP-binding protein).
GN OrderedLocusNames=SPY2194;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192694; PubMed=1196296; DOI=10.1073/pnas.071559398;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AB006636; AAK34822.1; -.
DR HSSP; Q58663; IGX.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30863 MW; DBE44F6F8780C7D5 CRC64;

Query Match 70.0%; Score 971; DB 2; Length 280;
Best Local Similarity 69.0%; Pred. No. 3.5e-59;
Matches 191; Conservative 35; Mismatches 51; Indels 0; Gaps 0;

QY 1 MGIALENVNTYQEGTTPLASAALSDVLTIEDGSYTALIGHTGSGKSTILQLLGLVPS 60
Db 1 MSINLQNVSYTYQAGTFPEGRALFNILDLGSYTAFIGHTGSGKSTIMQLLGLHVPT 60
QY 61 QGSVRVFDTLITSTSKNKDIRQKQVGLVFPQFAENQIPETVLKDVAFQPNFGVSEED 120
Db 61 TGIVSVDKQDITNHSKNKEIKSRKHVGLVFPQFESQLFEETVLKDVAFQPNFGVSP 120
QY 121 AVKTAREKALVGDIDSLFDRSPFELSGGOMRRVAIAGILAMEPAIILVLDPTAGLDPLG 180
Db 121 AEALAREKALVGISENLPFNKPFELSGGOMRRVAIAGILAMQPKVLVLDPTAGLDPLG 180
QY 181 RKELMTLFFKLHSGGMTIIVLTHLMDVVAIYANQVYVMEKGRVKGKPSDVFQDVVFME 240
Db 181 RRELMTLFFKLHSGGMTIIVLTHLMDVVAIYANQVYVMEKGRVKGKPSDVFQDVVFME 240
QY 241 EVOLGVPKITAFCKRLADRGVSFKLPIKIEEFKESL 277
Db 241 SKQLGVPKITQFAAHLRERGITFDALPITLEBFVEAIKNG 280
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QY 241 EVOLGVPKITAFCKRLADRGVSFKLPIKIEEFKESL 277
Db 241 KKQLGVPKVTAKLQRLVDRGIPISLPTLEBELREV 277

RESULT 5
Q7CMW8 PRELIMINARY; PRT; 280 AA.
AC Q7CMW8;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Putative ABC transporter (ATP-binding protein).
GN OrderedLocusNames=spym18 2229;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232;
RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Compel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AB010123; AAL98661.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30863 MW; DBE44F6F8780C7D5 CRC64;

Query Match 70.0%; Score 971; DB 2; Length 280;
Best Local Similarity 69.0%; Pred. No. 3.5e-59;
Matches 191; Conservative 35; Mismatches 51; Indels 0; Gaps 0;

QY 1 MGIALENVNTYQEGTTPLASAALSDVLTIEDGSYTALIGHTGSGKSTILQLLGLVPS 60
Db 1 MSINLQNVSYTYQAGTFPEGRALFNILDLGSYTAFIGHTGSGKSTIMQLLGLHVPT 60
QY 61 QGSVRVFDTLITSTSKNKDIRQKQVGLVFPQFAENQIPETVLKDVAFQPNFGVSEED 120
Db 61 TGIVSVDKQDITNHSKNKEIKSRKHVGLVFPQFESQLFEETVLKDVAFQPNFGVSP 120
QY 121 AVKTAREKALVGDIDSLFDRSPFELSGGOMRRVAIAGILAMEPAIILVLDPTAGLDPLG 180
Db 121 AEALAREKALVGISENLPFNKPFELSGGOMRRVAIAGILAMQPKVLVLDPTAGLDPLG 180
QY 181 RKELMTLFFKLHSGGMTIIVLTHLMDVVAIYANQVYVMEKGRVKGKPSDVFQDVVFME 240
Db 181 RRELMTLFFKLHSGGMTIIVLTHLMDVVAIYANQVYVMEKGRVKGKPSDVFQDVVFME 240
QY 241 EVOLGVPKITAFCKRLADRGVSFKLPIKIEEFKESL 277
Db 241 KKQLGVPKVTAKLQRLVDRGIPISLPTLEBELREV 277
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RESULT 6
Q8K5H2 PRELIMINARY; PRT; 280 AA.
ID Q8K5H2; Q79VY7;
AC 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Putative ABC transporter (ATP-binding protein).
GN OrderedLocNames=SPa1841, SpY3_1845;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OC NCBI_TaxID=198466;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=1212206; DOI=10.1073/pnas.152298499;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., Musser J.M.;
RA Schlievert P.M., McCormick J.K., Leung D.Y.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=SSI-1;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Taniyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution";
RL Genome Res. 13:1042-1055(2003).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AF014172; AAM80452.1; -.
DR EMBL; AF005146; BAC64936.1; -.
DR HSP; Q58663; 1G9X.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR Pfam; PF00005; ABC_tran_1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30905 MW; 8E7752BD48834752 CRC64;

Query Match 69.9%; Score 969; DB 2; Length 280;
Best Local Similarity 68.6%; Pred. No. 4.7e-59;
Matches 190; Conservative 36; Mismatches 51; Indels 0; Gaps 0;

QY 1 MGIALENNFTYQGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTILQLLNGLLVPS 60
Db 1 MGINLQNSYTYQVGTPEGRALFNILDLGSGYTAFTIGHTGSGKSTIMQLLNLHVP 60

QY 61 QGSVRVFDLTITSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGPNFGVSEED 120
Db 61 TGIVSVKQDIINSHSKNEIKSIRKHVGLVFPSPSQLFEETVLKDVAFGPNFGISPEE 120

QY 121 AVKTAREKALVIGIDESLPDRSPFELSGGQMRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
Db 121 TGIVSVKQDIINSHSKNEIKSIRKHVGLVFPSPSQLFEETVLKDVAFGPNFGISPEE 120

QY 181 RKLMTLFPKLLHQSGMTIVLTHLMDVAVYANQVYVMEKRLVKGKPSDFQDVVME 240
Db 181 ABALAREKALVIGISENLPKPNPFELSGGQMRVAIAGILAMQPKVLDDEPTAGLDPLG 180

QY 181 RKLMTLFPKLLHQSGMTIVLTHLMDVAVYANQVYVMEKRLVKGKPSDFQDVVME 240

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Db 181 RKLMTLFPKLLHQSGMTIVLTHLMDVAVYADVPVYLDKGIILSGPKTIQFOVSILLE 240
QY 241 EVQLGVPKITAFCKRLADRGVSPFKRLPIKIEEFKESL 277
Db 241 KKLQGVPKVTKLAQLVDRGIPISLSLITLLELREVL 277

RESULT 7
Q8DMR4 PRELIMINARY; PRT; 280 AA.
ID Q8DMR4
AC Q8DMR4;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ABC transporter, ATP-binding protein.
GN OrderedLocNames=SAG2150;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=216466;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tetelin H., Masignani V., Cielesiewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radu D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
RA Cardy H.A., Cline R.T., Van Aken S.E., Gill J.J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE014289; AAN01008.1; -.
DR HSP; P58301; 1US8.
DR TIGR; SAG2150; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 31111 MW; 00253EF4A7E5C30B CRC64;

Query Match 68.3%; Score 948; DB 2; Length 280;
Best Local Similarity 66.8%; Pred. No. 1.3e-57;
Matches 185; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

QY 1 MGIALENNFTYQGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTILQLLNGLLVPS 60
Db 1 MGISFKNYSYTYQAGTPEGRALFDVNLKIEDASVTAFTIGHTGSGKSTIMQLLNLHPT 60

QY 61 QGSVRVFDLTITSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGPNFGVSEED 120
Db 61 KGRVIVDDFSIKAGDNKEIKFIRKQVGLVFPFESQLFEETVLKDVAFGPNFGISQIE 120

QY 121 AVKTAREKALVIGIDESLPDRSPFELSGGQMRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
Db 121 AERLAEREKALVIGISEDLFDKNPFELSGGQMRVAIAGILAMEPKVLDDEPTAGLDPLG 180

QY 181 RKLMTLFPKLLHQSGMTIVLTHLMDVAVYANQVYVMEKRLVKGKPSDFQDVVME 240
Db 181 RKLMTLFPKLLHQSGMTIVLTHLMDVAVYADVPVYLDKGIILSGPKTIQFOVSILLE 240

QY 241 EVQLGVPKITAFCKRLADRGVSPFKRLPIKIEEFKESL 277

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Db 241 SKOLGVPKITKFAQLSHKGLNLSPLITINEFVEAI 277

RESULT 8

Q8E2L3 PRELIMINARY; PRT; 280 AA.

AC Q8E2L3; 280 AA.

AC Q8E2L3; 280 AA.

DT 01-MAR-2003 (T-EMBLrel. 23, Created)

DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Hypothetical protein gbs2109.

GN OrderedLocusNames=gbs2109;

OS Streptococcus agalactiae (serotype III).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=216495;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NEM316 / Serotype III;

MDLINE=2242508; PubMed=12354221;

RA Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,

RA Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trier-Cuot P.,

RA Kunst F.;

RT "Genome sequence of Streptococcus agalactiae, a pathogen causing

RT invasive neonatal disease.";

RL Mol. Microbiol. 45:1499-1513 (2002).

CC -1- SIMILARITY: Belongs to the ABC transporter family.

EMBL; AL766856; CAD47768.1; -.

DR HSP; P58301; IUS8.

DR Sagalict; gbs2109; -.

DR GO: 0016020; C:membrane; IEA.

DR GO: 0005524; F:ATP binding; IEA.

DR GO: 0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.

DR GO: 0000166; F:nucleotide binding; IEA.

DR GO: 0006810; P:transport; IEA.

DR InterPro; IPR003593; AAA ATPase.

DR Pfam; PF00005; ABC tran; 1.

DR ProDom; PD000006; ABC transporter; 1.

DR SMART; SM00382; AAA; 1.

DR PROSITE; PS00211; ABC TRANSPORTER_1; 1.

DR PROSITE; PS50893; ABC TRANSPORTER_2; 1.

KW ATP-binding; Complete proteome.

SK SEQUENCE 280 AA; 31111 MW; 00253EF4A7E5C30B CRC64;

Query Match 68.3%; Score 948; DB 2; Length 280;

Best Local Similarity 66.8%; Pred. No. 1.3e-57;

Matches 185; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

QY 1 MGIALENVNTYQEGTPLASALSDVSLTIEDGSGYALIGHTSGKSTILQLLGLLVP 60

DB 1 MGIEFNKVSYYQAGTFPEGRALFDNLKEDASYAFIGHTSGKSTIMQLLGLHPT 60

QY 61 QGSRVFDTLITSTSKNKDIRQIRKQVGLVFQFAENQIFETVLKDVAFQPNFGVSEED 120

DB 61 KGEVIVDDFSIKAGDKNKEIKFIRKQVGLVFQFPESQLFEETVLKDVAFQPNFGVSE 120

QY 121 AVKTAREKALVIGIDESLFRSPFELSGGQMRRAIAGILAMEPAILVLDEPTAGLDPLG 180

DB 121 AERLAEEKRLVIGISEDLPKPNFELSGGQMRRAIAGILAMEPAILVLDEPTAGLDPLG 180

QY 181 RKEMLTLPKHLQSGMTIVLTHLMDVADYAVYVLEKGRVKGKPSDVFQDVFMVE 240

DB 181 RKEMLTLPKHLQSGMTIVLTHLMDVADYAVYVLEKGRVKGKPSDVFQDVFMVE 240

QY 241 EVQLGVPKITAFCKRLADRGVSPFKRLPIKIEEFKESL 277

DB 241 SKOLGVPKITKFAQLSHKGLNLSPLITINEFVEAI 277

RESULT 9

OSCS8 PRELIMINARY; PRT; 288 AA.

AC Q9CIS8; 288 AA.

AC Q9CIS8; 288 AA.

DT 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE ABC transporter ATP-binding protein.

GN Name=ycheE; OrderedLocusNames=LL0278;

OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.

OX NCBI_TaxID=1360;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LL1403;

MDLINE=21235186; PubMed=11337471; DOI=10.1101/gr-GR-1697R;

RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,

RA Weissenbach J., Ehrlich S.D., Sorokin A.;

RT "The complete genome sequence of the lactic acid bacterium Lactococcus

RT lactis ssp. lactis IL1403.";

RL Genome Res. 11:731-753 (2001).

CC -1- SIMILARITY: Belongs to the ABC transporter family.

EMBL; AE006265; AAK04376.1; -.

DR PIR; F86659; F86659.

DR HSP; P58301; IUS8.

DR GO: 0016020; C:membrane; IEA.

DR GO: 0005524; F:ATP binding; IEA.

DR GO: 0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.

DR GO: 0000166; F:nucleotide binding; IEA.

DR GO: 0006810; P:transport; IEA.

DR InterPro; IPR003593; AAA ATPase.

DR InterPro; IPR003439; ABC transporter.

DR Pfam; PF00005; ABC tran; 1.

DR ProDom; PD000006; ABC transporter; 1.

DR SMART; SM00382; AAA; 1.

DR PROSITE; PS00211; ABC TRANSPORTER_1; 1.

DR PROSITE; PS50893; ABC TRANSPORTER_2; 1.

KW ATP-binding; Complete proteome.

SK SEQUENCE 288 AA; 31848 MW; 9326C417DE7AEF22 CRC64;

Query Match 64.9%; Score 899.5; DB 2; Length 288;

Best Local Similarity 64.8%; Pred. No. 3.1e-54;

Matches 173; Conservative 46; Mismatches 47; Indels 1; Gaps 1;

QY 3 IALENVNTYQEGTPLASALSDVSLTIEDGSGYALIGHTSGKSTILQLLGLLVP 62

DB 2 IKFEKVNYYQNSPFASRALFDIDLVKSGSYALIGHTSGKSTILQLLGLLVP 61

QY 63 SVRVFDTLITSTSKNKDIRQIRKQVGLVFQFAENQIFETVLKDVAFQPNFGVSEED 122

DB 62 TVRVGDIVTISTSKQKEIKFVRKKVGVVFPESQLFEETVLKDVAFQPNFGVSEED 121

QY 123 KTAREKALVIGIDESLFRSPFELSGGQMRRAIAGILAMEPAILVLDEPTAGLDPLGRK 182

DB 122 KIAAEKLEWGLSKPEWKSPELGGQMRRAIAGILAMEPAILVLDEPTAGLDPLKARI 181

QY 183 ELMTLPKHLQSGMTIVLTHLMDVADYAVYVLEKGRVKGKPSDVFQDVFMVE 242

DB 182 EMMKLPESHOTGQTIVLTHLMDVADYAVYVLEKGRVKGKPSDVFQDVFMVE 241

QY 243 QLGVPKITAFCKRLADRGV-SFKRLPI 268

DB 242 ELGVNPKATHPADQLQKTGYITFEKLP 268

RESULT 10

Q839D4 PRELIMINARY; PRT; 291 AA.

ID Q839D4; 291 AA.

AC Q839D4; 291 AA.

DT 01-JUN-2003 (T-EMBLrel. 24, Created)

DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE ABC transporter, ATP-binding protein.

GN OrderedLocusNames=EF0238;

OS Enterococcus faecalis (Streptococcus faecalis).

```
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerji L., Myers G.S.A., Nelson K.E., Sehadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis."
RL Science 299:2071-2074 (2003).
CC -I- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE016947; AA080106.1; -.
DR HSP; Q58206; 1L2T.
DR TIGR; EF0238; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS08993; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
KW SEQUENCE 291 AA; 32575 MW; F1E0DC04824B2F05 CRC64;

Query Match 61.3%; Score 850.5; DB 2; Length 291;
Best Local Similarity 57.9%; Pred. No. 7.5e-51;
Matches 161; Conservative 54; Mismatches 62; Indels 1; Gaps 1;

QY 1 MGIALENVFTYQEGTPLASALSVSITIEDGYSYALIGHTGSGKSTILQNLGLVPS 60
DB 3 MDIRKQVDFTQPTPEQRALFINLTQDSYTAIVGHTGSGKSTILQNLGLVPS 62
QY 61 QGSVRFDTLITSTSKNDIRKQVGLVFOFAENQIPFETVLKDVAFGPNQVGSSE 120
DB 63 KQQTIVGIRVITPTDNKNLKRIRKQVGLVFOFAENQIPFETVLKDVAFGPNQVGSSE 122
QY 121 AVKTAREKALVIGDESIFDRSPFELSGGQMRVAIAGILAMEPAIILVLDPTAGLDPLG 180
DB 123 AKKAKMLDLVGLDEKYLQHSFPFELSGGQMRVAIAGILAMEPAIILVLDPTAGLDPLG 182
QY 181 RKEMLTLFKKLH-QSGMTIVLVTHLMDVVAEYANQVYMEKGRLVKGGKPSDVQDVVFM 239
DB 183 RKEMMEMSRLKHEHMTIVLVTHLMDVVAEYANQVYMEKGRLVKGGKPSDVQDVVFM 240
QY 240 EVQGVGPKITAFCKRLADRGVSFKRLPIKIEFKESL 277
DB 243 KEKQLGVPPTAAEFAEKLVAKGFSFEQLPLTADQLADQL 280

RESULT 11
Q88XV1
AC Q88XV1; PRELIMINARY; PRT; 295 AA.
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ABC transporter, ATP-binding protein.
GN OrderedLocusNames=lp_1074;
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OX NCBI_TaxID=1590;

SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Sijzen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).
CC -I- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AL935254; CAD63607.1; -.
DR HSP; Q58663; 1G9X.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS08993; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
KW SEQUENCE 295 AA; 32302 MW; B3DC667CEB1E7949 CRC64;

Query Match 61.2%; Score 849.5; DB 2; Length 295;
Best Local Similarity 58.3%; Pred. No. 9e-51;
Matches 162; Conservative 52; Mismatches 63; Indels 1; Gaps 1;

QY 1 MGIALENVFTYQEGTPLASALSVSITIEDGYSYALIGHTGSGKSTILQNLGLVPS 60
DB 1 MAITFKQVDFTQPTPEKALTDINVITGYSYALIGHTGSGKSTILQNLGLVPS 60
QY 61 QGSVRFDTLITSTSKNDIRKQVGLVFOFAENQIPFETVLKDVAFGPNQVGSSE 120
DB 61 SGTIVGIRVITPTTSNKNLKRIRKQVGLVFOFAENQIPFETVLKDVAFGPNQVGSSE 120
QY 121 AVKTAREKALVIGDESIFDRSPFELSGGQMRVAIAGILAMEPAIILVLDPTAGLDPLG 180
DB 121 AKTAAEMALVIGDESILITSPFELSGGQMRVAIAGILAMEPAIILVLDPTAGLDPLG 180
QY 181 RKEMLTLFKKLH-QSGMTIVLVTHLMDVVAEYANQVYMEKGRLVKGGKPSDVQDVVFM 239
DB 181 RLDNMWMPARLRHERDLTVLVTHQMDVVAEYANQVYMEKGRLVKGGKPSDVQDVVFM 240
QY 240 EVQGVGPKITAFCKRLADRGVSFKRLPIKIEFKESL 277
DB 241 TAHQGLGPKTTAFATHTLQKQGMQFNWPLTEDELAAL 278

RESULT 12
P70970
ID P70970 PRELIMINARY; PRT; 276 AA.
AC P70970; Q79752;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein orf5 (yba5 protein).
GN Name=orf5; Synonyms=yba5; OrderedLocusNames=BSU01460;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]_TaxID=1423;
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97124188; PubMed=8969501;
RA Yasumoto K., Liu H., Jeong S.M., Ohashi Y., Kakinuma S., Tanaka K.,
RA Kawamura F., Yoshikawa H., Takahashi H.;
RT "Sequence analysis of a 50 kb region between spoOH and rrrH on the
```

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RT Bacillus subtilis chromosome. ";
RL Microbiology 142:3039-3046(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=980404033; PubMed=9384377; DOI=10.1038/36786;
RA Kunat F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Berto M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruchi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferraci E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haleb J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karanata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -I- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL: D64126; BAA10984.1; -.
DR EMBL: Z99104; CAB11922.1; -.
DR PIR: E69742; E69742.
DR HSSP: Q58663; 1G9X.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO: GO:0001666; F:nucleotide binding; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE: PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Hypothetical protein.
SQ SEQUENCE 276 AA; 30578 MW; A5AE1B64360016C9 CRC64;

Query Match 52.6%; Score 729; DB 2; Length 276;
Best Local Similarity 56.4%; Pred. No. 1.7e-42;
Matches 146; Conservative 45; Mismatches 66; Indels 2; Gaps 2;

QY 16 TPASAALSVSITIEDGSGYTAIHTGSGKSTILQNLGLVPSQGSVRVFDLTITSTS 75
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 TPPEALYDINASIKESGVAVVIGHTGSGKSTILQHLGLKPTKGQISLGSTVIQAGK 62
QY 76 KNKDRIKQVGLVFOFANQIFETVLKDVAFQNGFVSEDVAKTAKEKALVGLID 135
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 KNKDLKKLRKKGIVGFQFPHQLFEETVLKDISFGPNFVKKEDAEQKAREMLQLVGLS 122
QY 136 ESLFDRSPFELSGGQMRVAIAGLAMEPAILVLDDEPTAGLDPLGRKELMTLFKHLQSG 195
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 EELLDRSPFELSGGQMRVAIAGVLANDEPVVLVLDDEPTAGLDPRGRKEIMDMFVFLHQG 182

RESULT 14

QY 196 -MTIVLVTHLMDDDVAEYANQVYVMEKGRVLKGGKESDFVQDVVFMEEVQLGVPKITAFCK 254
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
193 NLTITLVTHSMEDAAAYADEMLVMEKGTIQASGSPRDLFLKGEEMAGWGLDLPETIKFQR 242
QY 255 RL-ADRGVSPFKRLPIKIEE 272
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
243 HLEAALGVFRNEPMLTIED 261

RESULT 13
Q65P76 PRELIMINARY; PRT; 289 AA.
AC Q65P76;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE YbaE (ABC transporter).
GN Name=ybaE; ORFNames=BL01022, BLi00164;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RX PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RA "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
RT Organism with Great Industrial Potential.";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaratsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berka R.M.;
RA "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL: AE017333; AAU39138.1; -.
DR EMBL: CP000002; AAU21793.1; -.
SQ SEQUENCE 289 AA; 32264 MW; 31B74C6C9B46A0AC CRC64;

Query Match 52.4%; Score 727; DB 2; Length 289;
Best Local Similarity 53.6%; Pred. No. 2.5e-42;
Matches 147; Conservative 50; Mismatches 75; Indels 2; Gaps 2;

QY 1 MGTALENVNTYQEGTPLASAALSVDLSLTEDGSGYTAIHTGSGKSTILQNLGLVPS 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MDIEIKDVEHYQMKTPFERLAIYDVAIVKESGVAVVIGHTGSGKSTILQHLGLKPT 60
QY 61 QGSVRVFDLTITSTSNNKDRIKQVGLVFOFANQIFETVLKDVAFQNGFVSEED 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 KQIIRLGEDVLEAGKNKHLKALKRKGIVGFQFPHQLFEETILKDIAGFPIFGMSREK 120
QY 121 AVKTAKEKALVGLIDSLFDRSPFELSGGQMRVAIAGLAMEPAILVLDDEPTAGLDPLG 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 AEBKAREMLKVLGLGAELSDRSPPFELSGGQMRVAIAGVLANDEPVVLVLDDEPTAGLDPRG 180
QY 181 RKELMTLFKHLH-QSGMTIVLVTHLMDDDVAEYANQVYVMEKGRVLKGGKESDFVQDVVFM 239
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 RKEIMDMFVSLHKQRLNLTITLVTHSMEDAAAYADEMLVMEKGTIQASGSPRDLFLKGEEMAGWGLDLPETIKFQR 242
QY 240 EEVQLGVPKITAFCKELADR-GVSKRRLPIKIEE 272
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
241 AALGLDLPETIKFCKELEETLGTITFKAPILTIEE 274

RESULT 14
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 18:07:29 ; Search time 40 Seconds

(without alignments)
671.112 Million cell updates/sec

Title: US-09-769-744D-26

Perfect score: 279

Sequence: 1 MGIALENVNTYQEGTPLAS.....GVSPKRLPIKIEFKESLNG 279

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	279	100.0	279	2	C95259
2	167	59.9	279	2	F98124
3	23	8.2	288	2	F86659
4	19	6.8	276	2	E69742
5	18	6.5	288	2	AH1399
6	18	6.5	288	2	AG1775
7	13	4.7	183	2	T44413
8	13	4.7	282	2	E83670
9	12	4.3	304	2	C90560
10	11	3.9	253	2	G72598
11	11	3.9	279	2	G64435
12	11	3.9	300	2	S34187
13	10	3.6	178	2	S77760
14	10	3.6	264	2	G83245
15	10	3.6	268	2	AG1225
16	10	3.6	268	2	A11578
17	10	3.6	271	2	AG0757
18	10	3.6	277	2	T45265
19	10	3.6	278	2	F87536
20	10	3.6	284	2	T35723
21	10	3.6	286	2	F97281
22	10	3.6	286	2	G82698
23	10	3.6	303	2	S62814
24	10	3.6	304	2	I64219
25	10	3.6	307	2	T36000
26	10	3.6	311	2	A69095
27	10	3.6	433	2	D82879
28	10	3.6	601	2	F83790
29	9	3.2	210	2	S76316

30	9	3.2	224	2	AE1999	ATP-binding protei
31	9	3.2	242	2	F84315	cobalt transport A
32	9	3.2	260	2	S75010	ABC-type transport
33	9	3.2	260	2	S74597	ABC-type transport
34	9	3.2	260	2	AD1829	ATP-binding protei
35	9	3.2	278	2	T44412	ABC transporter (A
36	9	3.2	280	2	T03543	probable cobalt tr
37	9	3.2	285	2	F69375	hypothetical prote
38	9	3.2	286	2	H90018	ABC transporter (A
39	9	3.2	288	2	D83731	ABC transporter syst
40	9	3.2	293	2	AI2139	ABC transporter, A
41	9	3.2	294	2	D87691	hypothetical prote
42	9	3.2	364	2	T02364	hypothetical prote
43	9	3.2	472	2	D98199	hypothetical prote
44	9	3.2	496	2	AE0305	probable sugar tra
45	9	3.2	500	2	AE3087	hypothetical prote
46	9	3.2	508	2	G95421	probable ABC trans
47	9	3.2	554	2	E70435	ABC transporter (M
48	9	3.2	565	2	E86665	ABC transporter AT
49	9	3.2	590	2	A84986	mdlb [imported] -
50	9	3.2	593	2	AI0559	probable ABC trans
51	9	3.2	593	2	A64775	ABC-type transport
52	9	3.2	593	2	G90691	ABC-type transport
53	9	3.2	605	2	S85542	ABC-type transport
54	9	3.2	607	2	AH0381	probable ATP trans
55	9	3.2	611	2	E86657	ABC transporter AT
56	9	3.2	697	2	G70704	hypothetical prote
57	9	3.2	724	2	B87015	ABC transporter ML
58	9	3.2	726	2	T44905	ABC-type transport
59	9	3.2	726	2	E70203	exonuclease Sbcc (
60	9	3.2	950	2	E70203	hypothetical mdl f
61	9	3.2	1143	4	I84547	genome polyprotein
62	9	3.2	2410	1	JQ1948	interleukin 12 p35
63	9	3.2	2412	1	JQ1537	cell division AP3
64	8	2.9	215	2	I56135	heme exporter prot
65	8	2.9	216	2	E81247	probable ureashort
66	8	2.9	222	2	AG3483	hypothetical prote
67	8	2.9	231	2	A96031	probable ATP-bindi
68	8	2.9	231	2	AH2872	polysaccharide ABC
69	8	2.9	231	2	B97649	ABC transporter AT
70	8	2.9	237	2	A69255	hypothetical prote
71	8	2.9	238	2	G96929	branched-chain ami
72	8	2.9	248	2	AG2969	hypothetical prote
73	8	2.9	248	2	G69352	oligopeptide trans
74	8	2.9	250	2	AG2885	ABC transporter, A
75	8	2.9	252	2	D97661	ABC transporter AT
76	8	2.9	259	2	F86843	ABC-type MDR trans
77	8	2.9	259	2	H97301	ferrichrome ABC tr
78	8	2.9	274	2	AH1319	glutamine ABC tran
79	8	2.9	274	2	AH1691	ABC transporter, A
80	8	2.9	275	2	D98313	spermidine/putresc
81	8	2.9	311	2	F87655	hypothetical prote
82	8	2.9	382	2	AG3533	hypothetical prote
83	8	2.9	385	2	F95161	hypothetical prote
84	8	2.9	385	2	E98027	probable oligopept
85	8	2.9	390	2	AE2576	hypothetical prote
86	8	2.9	420	2	C72720	hypothetical prote
87	8	2.9	428	2	C86770	oligopeptide trans
88	8	2.9	506	2	A82876	hypothetical prote
89	8	2.9	507	2	D98330	hypothetical prote
90	8	2.9	507	2	AI2952	sugar transport AT
91	8	2.9	510	2	AI0490	conserved hypothet
92	8	2.9	540	2	A82083	hypothetical prote
93	8	2.9	543	2	E89839	ABC transporter re
94	8	2.9	557	2	C84146	pept protein - Sta
95	8	2.9	571	2	S58356	probable amidase -
96	8	2.9	583	2	T39112	ABC transporter, A
97	8	2.9	583	2	G95214	hypothetical prote
98	8	2.9	583	2	F98078	probable ABC-trans
99	8	2.9	595	2	T31077	ABC transporter (A
100	8	2.9	601	2	AC1281	ABC transporter (A
101	8	2.9	601	2	AB1644	ABC transporter (A
102	8	2.9	601	2	AB1644	ABC transporter (A

103	8	2.9	606	2	JM0054	amiloride-sensitiv	176	7	2.5	276	2	T36288	probable ABC-type
104	8	2.9	606	2	AC2425	ATP-binding protei	177	7	2.5	277	2	E71545	probable oligopept
105	8	2.9	608	2	H86783	hypothetical prote	178	7	2.5	278	2	E65020	ethanolamine utili
106	8	2.9	636	2	C81128	ABC transporter, A	179	7	2.5	278	2	D91043	ethanolamine utili
107	8	2.9	646	1	E71536	probable transporter	180	7	2.5	278	2	G85887	ethanolamine utili
108	8	2.9	650	2	A11333	ABC transporter (A	181	7	2.5	279	2	AC0814	probable ethanolam
109	8	2.9	650	2	AH1704	ABC transporter (A	182	7	2.5	279	2	E97068	cobalt transport (
110	8	2.9	673	2	H69828	ABC transporter (A	183	7	2.5	279	2	AH1359	ABC transporter (A
111	8	2.9	674	2	F83794	ABC transporter (A	184	7	2.5	279	2	AH1775	ABC transporter (A
112	8	2.9	677	2	T10657	probable ABC-type	185	7	2.5	280	2	G75082	phosphate abc tran
113	8	2.9	680	2	T10656	probable ABC-type	186	7	2.5	280	2	G69043	cobalt transporter A
114	8	2.9	690	2	S54211	ATM1 protein precu	187	7	2.5	280	2	H75151	abc transporter, A
115	8	2.9	820	2	B83739	exinuclease ABC (188	7	2.5	283	2	E82662	ABC transporter AT
116	8	2.9	1323	2	T18214	ATP binding cassel	189	7	2.5	284	2	F81563	peptide ABC transp
117	7	2.5	89	1	S38882	ribosomal protein	190	7	2.5	284	2	G72107	oligopeptide trans
118	7	2.5	95	2	H69341	conserved hypothet	191	7	2.5	284	2	A86516	oligopeptide trans
119	7	2.5	104	2	T36976	probable transposa	192	7	2.5	284	2	S62839	sulfate transport
120	7	2.5	134	2	T36750	probable gntR-fami	193	7	2.5	284	2	T14167	ABC transport prot
121	7	2.5	143	2	B69782	hypothetical prote	194	7	2.5	284	2	G71192	probable Cobalt tr
122	7	2.5	150	2	B98044	ABC transporter, t	195	7	2.5	285	2	E87517	pantoate-beta-alan
123	7	2.5	153	2	C46036	ERK2 homolog - fru	196	7	2.5	292	2	H69999	ABC transporter (A
124	7	2.5	162	2	T16163	hypothetical prote	197	7	2.5	294	2	E82879	ABC transporter UU
125	7	2.5	174	2	G95096	DNA topology modul	198	7	2.5	305	2	F82303	ABC transporter, A
126	7	2.5	176	2	A72484	hypothetical prote	199	7	2.5	306	2	T36764	probable ABC-type
127	7	2.5	176	2	G70658	probable aroK prot	200	7	2.5	307	2	F87952	protein T2683.4 li
128	7	2.5	181	2	B70704	probable rocd - My	201	7	2.5	307	2	C83188	probable ATP-bind
129	7	2.5	183	2	A12926	conserved hypothet	202	7	2.5	308	2	D80524	hypothetical ABC t
130	7	2.5	183	2	F98355	hypothetical prote	203	7	2.5	308	2	B97589	probable ATP-bind
131	7	2.5	197	2	C69877	adenylsulfate ki	204	7	2.5	308	2	A12810	hypothetical prote
132	7	2.5	200	2	AD3220	conserved hypothet	205	7	2.5	308	2	H64980	hypothetical ABC t
133	7	2.5	201	2	F97035	p-loop kinase (uri	206	7	2.5	308	2	S45204	probable ABC-type
134	7	2.5	206	2	H84978	adenylsulfate k	207	7	2.5	308	2	C85496	hypothetical prote
135	7	2.5	206	2	AF2299	cobalt transport A	208	7	2.5	308	2	C90645	hypothetical prote
136	7	2.5	208	2	A84073	adenylsulfate ki	209	7	2.5	308	2	H85850	hypothetical prote
137	7	2.5	209	2	E64172	hypothetical prote	210	7	2.5	308	2	A91005	hypothetical prote
138	7	2.5	230	2	D69858	ABC transporter (A	211	7	2.5	308	2	AH0413	probable ABC trans
139	7	2.5	231	2	AG3225	hypothetical prote	212	7	2.5	309	2	T35756	probable branched
140	7	2.5	232	2	AE2049	ATP-binding protei	213	7	2.5	310	2	G82707	ABC transporter AT
141	7	2.5	233	2	B81076	thermonuclease fam	214	7	2.5	310	2	B83294	probable ATP-bind
142	7	2.5	237	2	A72688	probable high-affi	215	7	2.5	311	2	B95202	methionyl-tRNA for
143	7	2.5	238	2	B84967	hypothetical prote	216	7	2.5	311	2	B98069	methionyl-tRNA for
144	7	2.5	240	2	A11532	two-component resp	217	7	2.5	311	2	AC1158	ABC transporter (A
145	7	2.5	240	2	T25299	hypothetical prote	218	7	2.5	311	2	AH1516	ABC transporter (A
146	7	2.5	240	2	D74415	zinc ABC transport	219	7	2.5	312	2	G97382	probable ATP-bind
147	7	2.5	246	2	A69666	Na+ ABC transporte	220	7	2.5	312	2	AF2600	hypothetical prote
148	7	2.5	249	2	AF3225	hypothetical prote	221	7	2.5	312	2	AC0147	probable ABC trans
149	7	2.5	251	2	D85798	hypothetical prote	222	7	2.5	313	2	E70871	hypothetical prote
150	7	2.5	251	2	AH0742	high-affinity zinc	223	7	2.5	314	2	A39374	Renilla-luciferin
151	7	2.5	251	2	H75586	probable urea/shor	224	7	2.5	314	2	B75076	daunorubicin resis
152	7	2.5	251	2	H90949	probable ABC trans	225	7	2.5	314	2	C87667	ABC transporter, A
153	7	2.5	251	2	B64948	probable ABC trans	226	7	2.5	315	2	F90396	conserved hypothet
154	7	2.5	253	2	H89795	hypothetical prote	227	7	2.5	315	2	A82655	phage-related prot
155	7	2.5	253	2	AD0251	high-affinity zinc	228	7	2.5	315	2	A10777	ABC transporter AT
156	7	2.5	254	2	G72687	probable high-affi	229	7	2.5	315	2	S72783	probable ABC-type
157	7	2.5	255	2	G90403	conserved hypothet	230	7	2.5	316	2	B90282	hypothetical prote
158	7	2.5	255	2	C89936	hypothetical prote	231	7	2.5	316	2	S19389	hypothetical prote
159	7	2.5	255	2	F70501	probable ABC-type	232	7	2.5	318	2	S70973	hpf protein - Esc
160	7	2.5	257	2	B64458	high-affinity bran	233	7	2.5	319	2	E86861	methionyl-tRNA for
161	7	2.5	258	2	H42004	copper transport A	234	7	2.5	319	2	B53290	oligopeptide trans
162	7	2.5	260	2	T15237	hypothetical prote	235	7	2.5	320	2	S18444	G protein-coupled
163	7	2.5	260	2	B71234	probable transport	236	7	2.5	323	2	F75202	dipeptide abc tran
164	7	2.5	261	2	E69159	hypothetical prote	237	7	2.5	324	2	G89934	hypothetical prote
165	7	2.5	261	2	AB2952	hypothetical prote	238	7	2.5	324	2	T35090	probable ABC trans
166	7	2.5	261	2	C98331	probable peptide A	239	7	2.5	328	2	G64901	ABC-type transport
167	7	2.5	264	2	AB2904	hypothetical prote	240	7	2.5	328	2	A85728	hypothetical prote
168	7	2.5	264	2	G97679	probable ATP-bind	241	7	2.5	328	2	H90889	hypothetical prote
169	7	2.5	266	2	B97686	regulator protein	242	7	2.5	330	2	F72428	oligopeptide ABC t
170	7	2.5	266	2	AD2911	transcription regu	243	7	2.5	331	2	C72424	oligopeptide ABC t
171	7	2.5	266	2	A72401	ABC transporter, A	244	7	2.5	333	2	AC1209	teichoic acid tran
172	7	2.5	268	2	B64066	probable ABC trans	245	7	2.5	334	2	C87272	teichoic acid tran
173	7	2.5	269	2	A99919	hypothetical prote	246	7	2.5	335	2	AF1565	ATP-binding protei
174	7	2.5	274	2	H64219	hemolysin secretio	247	7	2.5	335	2	AE2354	ABC transporter AT
175	7	2.5	274	2	S62815	sulfate transport	248	7	2.5	339	2	AE2102	

249	7	2.5	339	2	A13609	daunorubicin resis	322	7	2.5	497	2	C34469	pule protein - Kle
250	7	2.5	340	2	T47019	hypothetical prote	323	7	2.5	498	2	S32859	outB protein - Erw
251	7	2.5	340	2	AF0236	probable glutamina	324	7	2.5	501	2	T00213	type II secretion
252	7	2.5	341	2	E65080	hypothetical prote	325	7	2.5	501	2	S22669	hypothetical prote
253	7	2.5	341	2	B91107	probable protein t	326	7	2.5	503	2	JU0147	general secretion
254	7	2.5	341	2	E85952	probable protein t	327	7	2.5	503	2	JN0524	tecpT protein - Vib
255	7	2.5	343	2	A10131	ABC transporter AT	328	7	2.5	503	2	F82275	toxin co-regulated
256	7	2.5	343	2	A95224	ABC transporter, A	329	7	2.5	503	2	AE0100	general secretion
257	7	2.5	343	2	D98088	hypothetical prote	330	7	2.5	513	2	C95089	ABC transporter, A
258	7	2.5	344	2	H82656	twitching motility	331	7	2.5	513	2	F97956	hypothetical prote
259	7	2.5	344	2	H82656	twitching motility	332	7	2.5	518	2	D69813	ABC transporter (A
260	7	2.5	345	2	F82321	twitching motility	333	7	2.5	519	2	D81293	probable type II p
261	7	2.5	346	2	G86262	hypothetical prote	334	7	2.5	522	2	JC1204	vga protein - Stap
262	7	2.5	347	2	B81243	twitching motility	335	7	2.5	523	2	S61017	hypothetical prote
263	7	2.5	347	2	C82016	probable pilus ret	336	7	2.5	524	2	F75610	histidine ammonia-
264	7	2.5	351	2	S74729	carboxysome format	337	7	2.5	528	1	WMBV88	58K protein - barl
265	7	2.5	351	2	S74729	carboxysome format	338	7	2.5	533	2	E64626	ABC transporter, A
266	7	2.5	352	2	T24154	hypothetical prote	339	7	2.5	533	2	H71886	probable ABC trans
267	7	2.5	352	2	E97108	pilT ATPase involv	340	7	2.5	534	2	S70971	hypothetical prote
268	7	2.5	353	2	JC7661	G protein alpha su	341	7	2.5	535	2	D90077	GCN20-2 protein -
269	7	2.5	353	2	S71965	GTP-binding regula	342	7	2.5	535	2	S56147	hypothetical prote
270	7	2.5	353	2	T50482	G protein alpha ch	343	7	2.5	540	2	A95264	hypothetical prote
271	7	2.5	353	2	S56262	hypothetical prote	344	7	2.5	540	2	AH3032	ABC transporter, A
272	7	2.5	354	2	S46245	RAE-30 protein - m	345	7	2.5	542	2	B87373	conserved hypothet
273	7	2.5	354	2	S74323	ABC-type transport	346	7	2.5	546	2	H87425	probable ABC trans
274	7	2.5	355	2	T50479	G protein alpha ch	347	7	2.5	547	2	T35267	endopeptidase IV-r
275	7	2.5	358	2	AD0115	conserved hypothet	348	7	2.5	556	2	F75315	ABC transporter, A
276	7	2.5	359	2	B70534	probable ribonucle	349	7	2.5	560	2	A95056	hypothetical prote
277	7	2.5	360	2	C72263	motility protein p	350	7	2.5	560	2	F97925	general secretion
278	7	2.5	361	2	T12470	hypothetical prote	351	7	2.5	566	2	A72329	hypothetical prote
279	7	2.5	366	2	C70365	twitching motility	352	7	2.5	566	2	D92058	mxid protein - Shi
280	7	2.5	368	2	G82321	twitching motility	353	7	2.5	567	2	D98253	hypothetical prote
281	7	2.5	370	1	A69396	probable ribose AB	354	7	2.5	571	2	H82355	peptide ABC transp
282	7	2.5	370	2	C82553	homoserine O-acety	355	7	2.5	573	2	AF1418	ABC transporter, A
283	7	2.5	370	2	F70484	twitching motility	356	7	2.5	573	2	AH1793	ABC transporter, A
284	7	2.5	370	2	B81945	probable pilus ret	357	7	2.5	573	2	E69802	ABC transporter (A
285	7	2.5	370	2	B81159	arabinose ABC tran	358	7	2.5	573	2	A82231	transport ATP-bind
286	7	2.5	371	2	B90489	twitching motility	359	7	2.5	574	2	T27100	hypothetical prote
287	7	2.5	374	2	S32916	pilT protein - Nei	360	7	2.5	575	2	C83313	probable type II s
288	7	2.5	376	2	AC3535	dipeptide transpor	361	7	2.5	575	2	D84146	ABC transporter re
289	7	2.5	376	2	G82656	twitching motility	362	7	2.5	575	2	JC4554	ATP-binding caaset
290	7	2.5	377	1	MFN285	matrix protein - s	363	7	2.5	576	2	D98834	MDR-type ABC trans
291	7	2.5	377	2	S74628	hypothetical prote	364	7	2.5	576	2	A97239	proteinase SM tran
292	7	2.5	383	1	A87049	probable phosphoes	365	7	2.5	576	2	A49933	ABC transporter, A
293	7	2.5	386	2	S68016	ATPase/RNA helicase	366	7	2.5	577	2	E72396	ABC transporter, A
294	7	2.5	399	2	B82723	carbamoyl-phosphat	367	7	2.5	577	2	C72275	phosphate response
295	7	2.5	403	1	C69213	protein-export mem	368	7	2.5	579	2	A27650	ABC transporter, A
296	7	2.5	403	2	F72254	hypothetical prote	369	7	2.5	580	2	AE1452	probable transport
297	7	2.5	408	2	A81243	twitching motility	370	7	2.5	582	2	AF0614	hypothetical prote
298	7	2.5	408	2	D82016	pilT-like protein	371	7	2.5	582	2	A70755	ATP-binding transp
299	7	2.5	420	2	B75333	twitching motility	372	7	2.5	582	2	S27998	probable ABC-type
300	7	2.5	421	2	AB2959	exopolysaccharide	373	7	2.5	582	2	C85617	ATP-binding transp
301	7	2.5	423	2	D98324	exopolysaccharide	374	7	2.5	582	2	D82146	transport ATP-bind
302	7	2.5	427	2	AC1394	human N-acetylgluc	375	7	2.5	582	2	AE0170	probable transport
303	7	2.5	427	2	AF1769	weakly human N-ace	376	7	2.5	584	2	E97303	hypothetical prote
304	7	2.5	428	2	S76184	hypothetical prote	377	7	2.5	584	2	D87048	ABC-type transport
305	7	2.5	432	2	AB2222	twitching motility	378	7	2.5	586	2	T48672	ATP-binding protei
306	7	2.5	437	2	T18555	ATP-binding protei	379	7	2.5	586	2	AH2133	hypothetical prote
307	7	2.5	438	2	AG2592	thymidine phosphor	380	7	2.5	586	2	F90044	hypothetical prote
308	7	2.5	438	2	A97375	thymidine phosphor	381	7	2.5	587	2	AD3122	probable ABC trans
309	7	2.5	446	2	B83033	probable MFS trans	382	7	2.5	587	2	AD3122	probable ABC trans
310	7	2.5	448	2	H70320	transcription regu	383	7	2.5	587	2	C98165	probable ABC-type
311	7	2.5	451	2	A83145	probable transport	384	7	2.5	587	2	H64045	probable ABC trans
312	7	2.5	452	2	S07886	site-specific DNA-	385	7	2.5	588	2	A10381	moab protein limpo
313	7	2.5	460	2	D75610	probable peroxidase	386	7	2.5	588	2	T45539	hypothetical prote
314	7	2.5	465	2	H90508	cobryic acid synth	387	7	2.5	589	2	H84985	probable ABC trans
315	7	2.5	475	2	D71871	DNA transfer prote	388	7	2.5	590	2	AH0559	ABC-type transport
316	7	2.5	481	2	S47441	transport protein	389	7	2.5	590	2	H64774	ATP-binding compon
317	7	2.5	490	2	G85354	hypothetical prote	390	7	2.5	590	2	F90691	ATP-binding compon
318	7	2.5	491	2	E97159	general secretion	391	7	2.5	590	2	B85542	ABC-type transport
319	7	2.5	492	2	B72389	shikimate kinase/3	392	7	2.5	593	2	S75352	ATP-binding protei
320	7	2.5	493	2	A65126	probable general s	393	7	2.5	597	2	AD2074	hypothetical prote
321	7	2.5	495	2	T11228	NADH2 dehydrogenas	394	7	2.5	598	2	T05329	hypothetical prote

395	7	2.5	598	2	T24717	hypothetical prote	468	7	2.5	1196	2	S65245	translation elonga
396	7	2.5	599	2	G83941	ABC transporter (A	469	7	2.5	1215	2	S65245	autoantigen - huma
397	7	2.5	600	2	B38875	two-component sens	470	7	2.5	1238	2	T18940	multidrug resistanc
398	7	2.5	603	2	AD2397	ATP-binding protei	471	7	2.5	1245	2	G86404	probable P-glycopr
399	7	2.5	604	2	A69858	ABC transporter (A	472	7	2.5	1247	2	S86405	probable P-glycopr
400	7	2.5	604	2	G95281	probable ABC trans	473	7	2.5	1269	2	S35366	furin (EC 3.4.21.7
401	7	2.5	606	2	T29190	hypothetical prote	474	7	2.5	1283	2	T18939	hypothetical prote
402	7	2.5	606	2	C88174	hypothetical ABC t	475	7	2.5	1307	2	T30882	multidrug resistanc
403	7	2.5	606	2	AB3113	hypothetical prote	476	7	2.5	1327	2	T41647	probable pre-mrna
404	7	2.5	609	2	AF2379	protease IV (imp	477	7	2.5	1345	2	A87102	probable SpoIIIE-f
405	7	2.5	609	2	E96742	probable ABC trans	478	7	2.5	1355	2	T00961	hypothetical prote
406	7	2.5	609	2	A81245	D-1-deoxyxylulose	479	7	2.5	1362	2	T41534	leptomycin B resis
407	7	2.5	613	2	AD0796	NADH2 dehydrogenas	480	7	2.5	1407	1	T00558	probable ABC trans
408	7	2.5	614	2	D64630	hypothetical prote	481	7	2.5	1408	2	T47671	P-glycoprotein-li
409	7	2.5	614	2	B11884	hypothetical prote	482	7	2.5	1419	1	DVZQF	multidrug resistanc
410	7	2.5	619	2	T17193	probable protoporp	483	7	2.5	1427	2	T39219	atp-binding cassel
411	7	2.5	620	1	I39755	adenyl-sulfate k	484	7	2.5	1431	2	T22748	hypothetical prote
412	7	2.5	622	2	T95377	hypothetical prote	485	7	2.5	1435	2	S59384	hypothetical prote
413	7	2.5	623	2	P69093	RNase L inhibitor	486	7	2.5	1447	2	T15200	hypothetical prote
414	7	2.5	630	2	D97669	hypothetical prote	487	7	2.5	1450	2	JC6139	cystic fibrosis tr
415	7	2.5	630	2	A12893	hypothetical prote	488	7	2.5	1451	2	T30821	P-glycoprotein - S
416	7	2.5	630	2	D95937	probable mureinpep	489	7	2.5	1469	2	T50210	probable ABC trans
417	7	2.5	632	2	A11607	D-1-deoxyxylulose	490	7	2.5	1472	2	B54774	ATP binding cassel
418	7	2.5	632	2	E97270	ATPase component o	491	7	2.5	1476	1	A39901	cystic fibrosis tr
419	7	2.5	633	2	H95932	probable adenyl-s	492	7	2.5	1476	1	A40303	cystic fibrosis tr
420	7	2.5	633	2	E97999	hypothetical prote	493	7	2.5	1480	1	DVHUCF	cystic fibrosis tr
421	7	2.5	633	2	H95128	ABC transporter, A	494	7	2.5	1481	1	A39323	CFTCR protein - Afr
422	7	2.5	635	2	F86757	ABC transporter, A	495	7	2.5	1485	2	S23756	multi resistance p
423	7	2.5	639	2	G82194	ABC transporter, A	496	7	2.5	1490	2	T47840	multi resistance p
424	7	2.5	640	2	H83267	probable ATP-bind	497	7	2.5	1514	2	T52080	MRP-like ABC trans
425	7	2.5	641	1	Z228N0	adenyl-sulfate k	498	7	2.5	1515	2	T52081	glutathione-conjug
426	7	2.5	641	2	E95320	adenyl-sulfate k	499	7	2.5	1516	2	P84919	ATP-binding cassel
427	7	2.5	641	2	F81408	ABC-type transmem	500	7	2.5	1529	2	A59189	ATP-binding cassel
428	7	2.5	651	2	A83230	hydantoin utilizat	501	7	2.5	1534	2	T30295	P-glycoprotein - T
429	7	2.5	656	2	S30483	pol polyprotein -	502	7	2.5	1539	2	T48059	ABC transporter-li
430	7	2.5	660	2	P98020	hypothetical prote	503	7	2.5	1548	1	DVLNS	multidrug resistanc
431	7	2.5	672	2	S74374	general secretion	504	7	2.5	1564	2	T27121	hypothetical prote
432	7	2.5	692	2	T03377	homeotic protein H	505	7	2.5	1576	2	S65774	homeotic protein H
433	7	2.5	695	2	S51433	MDL1 protein - yea	506	7	2.5	1677	2	T18344	P-glycoprotein E -
434	7	2.5	705	2	B75371	ABC transporter, A	507	7	2.5	1704	2	T42749	ATP-binding cassel
435	7	2.5	708	2	C86404	probable protein A	508	7	2.5	1724	2	T18343	P-glycoprotein - S
436	7	2.5	712	2	S19387	saccharolysin (EC	509	7	2.5	1751	2	T50002	hypothetical prote
437	7	2.5	712	2	G62058	ABC transporter AT	510	7	2.5	1758	2	P88559	protein C48B4.4b [
438	7	2.5	719	2	S62466	probable ATP-depen	511	7	2.5	1767	2	S60124	transport protein
439	7	2.5	727	2	F82634	cell-specific prot	512	7	2.5	2201	2	A54774	ATP binding cassel
440	7	2.5	733	2	T22813	hypothetical prote	513	7	2.5	2269	2	T18472	hypothetical prote
441	7	2.5	735	2	S37903	probable ATP-depen	514	7	2.5	2322	2	T10542	hypothetical prote
442	7	2.5	744	2	T20969	hypothetical prote	515	7	2.5	2672	2	A48126	translation activa
443	7	2.5	747	2	S35546	ATP-dependent RNA	516	7	2.5	2970	2	T08839	polyprotein - marm
444	7	2.5	752	2	S56146	GCN20 protein - ye	517	7	2.5	3005	2	T08841	polyprotein - dour
445	7	2.5	757	2	B75437	ABC transporter, A	518	7	2.5	3010	1	A45573	genome polyprotein
446	7	2.5	781	2	A85035	hypothetical prote	519	7	2.5	3010	1	GNWVCU	genome polyprotein
447	7	2.5	787	2	E71984	DNA transfer prote	520	7	2.5	3010	1	GNWVTC	genome polyprotein
448	7	2.5	787	2	A64522	virB4 homolog - He	521	7	2.5	3010	1	GNWVTW	genome polyprotein
449	7	2.5	790	1	S77032	ABC transporter sl	522	7	2.5	3010	1	S18030	genome polyprotein
450	7	2.5	798	2	S34023	TATA box-binding p	523	7	2.5	3011	1	GNWVC3	genome polyprotein
451	7	2.5	822	2	AD3232	conjugal transfer	524	7	2.5	3011	1	GNWVCH	genome polyprotein
452	7	2.5	832	2	B87673	ABC transporter, H	525	7	2.5	3011	1	S40770	genome polyprotein
453	7	2.5	863	2	C90482	ABC transporter, A	526	7	2.5	3014	1	JC5620	genome polyprotein
454	7	2.5	923	2	H64081	ATP-dependent heli	527	7	2.5	3033	1	GNWVJ8	genome polyprotein
455	7	2.5	932	2	B70929	hypothetical prote	528	7	2.5	3033	1	J01303	genome polyprotein
456	7	2.5	938	2	T05533	hypothetical prote	529	7	2.5	4131	2	T21085	hypothetical prote
457	7	2.5	945	2	JN0901	endopeptidase Clp	530	6	2.2	13	2	S09018	hemolytic protein
458	7	2.5	962	1	JT0669	helicase II-like p	531	6	2.2	24	2	S56000	guanine kinase M
459	7	2.5	1019	2	T29623	hypothetical prote	532	6	2.2	28	2	S16228	gene Bta protein
460	7	2.5	1025	2	T31014	hypothetical prote	533	6	2.2	28	2	I46921	aryl acylamidase -
461	7	2.5	1025	2	T18376	hypothetical prote	534	6	2.2	44	2	G69861	conserved hypothet
462	7	2.5	1034	2	T30331	multidrug resistanc	535	6	2.2	50	2	S61922	gene bap1(3) prote
463	7	2.5	1037	2	T50518	P-glycoprotein - T	536	6	2.2	55	2	UJ0359	hypothetical prote
464	7	2.5	1057	2	T38694	ABC transporter-li	537	6	2.2	56	2	T70665	MHC HLA-A24 cell s
465	7	2.5	1085	2	G89056	probable translati	538	6	2.2	58	2	E36491	phosphoprotein pho
466	7	2.5	1165	2	D72496	hypothetical prote	539	6	2.2	58	2	G36491	phosphoprotein pho
467	7	2.5	1194	1	G70837	probable ABC trans	540	6	2.2	58	2	C87333	hypothetical prote

541	6	2.2	66	2	S03443	dnak-type molecule	614	6	2.2	143	2	AD1693	hypothetical prote
542	6	2.2	75	2	T08508	trbK protein - Ent	615	6	2.2	144	2	G70894	hypothetical prote
543	6	2.2	75	2	S53102	hypothetical prote	616	6	2.2	145	2	AE1399	ribosomal protein
544	6	2.2	75	2	A97799	hypothetical prote	617	6	2.2	145	2	AD1775	ribosomal protein
545	6	2.2	76	2	S26642	replication licens	618	6	2.2	146	1	CUNLBF	blue copper protei
546	6	2.2	77	2	H91094	hypothetical prote	619	6	2.2	146	2	TS1473	calmodulin-like pr
547	6	2.2	77	2	H86399	protein F17L21.12	620	6	2.2	146	2	E70845	hypothetical prote
548	6	2.2	77	2	D85940	hypothetical prote	621	6	2.2	146	2	AF2642	conserved hypotet
549	6	2.2	78	2	S52172	replication licens	622	6	2.2	148	2	C82799	single-stranded DN
550	6	2.2	80	2	F83997	exodeoxyribonuclea	623	6	2.2	148	2	B88933	ribosomal protein
551	6	2.2	80	2	F86027	hypothetical prote	624	6	2.2	148	2	AE1594	hypothetical prote
552	6	2.2	80	2	AE2529	hypothetical prote	625	6	2.2	148	2	HT1007	hypothetical prote
553	6	2.2	82	2	AG0713	probable membrane	626	6	2.2	149	2	E69653	transcription regu
554	6	2.2	82	2	C64940	transglycosylase-a	627	6	2.2	149	2	D82178	hypothetical prote
555	6	2.2	82	2	H85790	transglycosylase-a	628	6	2.2	151	2	H82654	single-stranded DN
556	6	2.2	82	2	H90941	transglycosylase-a	629	6	2.2	152	2	F64441	molybdenum cofacto
557	6	2.2	82	2	JT0765	rapid lysis III pr	630	6	2.2	152	2	AC0286	conserved hypotet
558	6	2.2	86	2	E95225	hypothetical prote	631	6	2.2	152	2	H63376	hypothetical prote
559	6	2.2	86	2	H98089	hypothetical prote	632	6	2.2	154	2	T04159	histone H1 homolog
560	6	2.2	88	2	H86752	prophage p12 prote	633	6	2.2	155	2	F45831	MHC class I histoc
561	6	2.2	89	2	D83052	30S ribosomal prot	634	6	2.2	155	2	S70046	hypothetical prote
562	6	2.2	90	2	T04077	probable ribosomal	635	6	2.2	155	2	T21364	hypothetical prote
563	6	2.2	90	2	AD1606	hypothetical prote	636	6	2.2	156	2	E84991	30S ribosomal prot
564	6	2.2	90	2	AH1243	hypothetical prote	637	6	2.2	156	2	C86626	hypothetical prote
565	6	2.2	91	2	A46685	GTP-binding regula	638	6	2.2	157	2	G97424	hypothetical prote
566	6	2.2	93	2	AC0081	conserved hypotet	639	6	2.2	157	2	AC2405	conserved hypotet
567	6	2.2	94	2	E45831	MHC class I histoc	640	6	2.2	158	2	G70323	gene 60 protein -
568	6	2.2	96	2	G86801	prophage p13 prote	641	6	2.2	159	1	W2BE60	H+-transporting tw
569	6	2.2	100	2	F82453	conserved hypotet	642	6	2.2	159	2	S28959	probable molybdenu
570	6	2.2	106	2	A71193	hypothetical prote	643	6	2.2	159	2	C71192	molybdenum cofacto
571	6	2.2	107	2	AC0145	probable membrane	644	6	2.2	159	2	E75151	hypothetical prote
572	6	2.2	108	2	S67638	forkehead transcrip	645	6	2.2	160	2	C64353	hypothetical prote
573	6	2.2	108	2	A48524	forkehead transcrip	646	6	2.2	160	2	S77246	probable signal pe
574	6	2.2	110	2	AB1526	ABC transporter, A	648	6	2.2	161	2	D90273	phosphohistidine p
575	6	2.2	110	2	AF3331	cobalt transport A	649	6	2.2	162	2	C64482	hypothetical prote
576	6	2.2	111	2	B85965	hypothetical prote	650	6	2.2	162	2	E90275	thermoresistant gl
577	6	2.2	111	2	F72267	hypothetical prote	651	6	2.2	163	2	E97382	glucosyltransferase
578	6	2.2	113	2	I73679	phosphoprotein pho	652	6	2.2	163	2	AD2600	photosystem I chai
579	6	2.2	114	2	D36769	14R protein - huma	653	6	2.2	164	2	S22204	shikimate kinase (
580	6	2.2	114	2	C90344	hypothetical prote	654	6	2.2	165	2	S22204	probable cdc2-like
581	6	2.2	115	2	D70123	ribosomal protein	655	6	2.2	166	2	T12201	stress related pro
582	6	2.2	115	2	S77435	hypothetical prote	656	6	2.2	167	2	T11750	thiol peroxidase (
583	6	2.2	115	2	F75284	hypothetical prote	657	6	2.2	168	2	AG0659	ferritin (imported
584	6	2.2	116	2	S16361	GTP-binding protei	658	6	2.2	169	2	AE0217	2',3'-cyclic-nucle
585	6	2.2	116	2	H65091	hypothetical prote	659	6	2.2	169	2	T49618	Ig heavy chain V r
586	6	2.2	117	2	I57454	MHC class I antige	660	6	2.2	171	2	S23623	hypothetical prote
587	6	2.2	118	2	AC0891	conserved hypotet	661	6	2.2	171	2	B71147	thermoresistant gl
588	6	2.2	118	2	AG1004	conserved hypotet	662	6	2.2	172	2	B75338	transcription repr
589	6	2.2	118	2	T01246	30S ribosomal prot	663	6	2.2	173	2	B39141	conserved hypotet
590	6	2.2	119	2	B91120	hypothetical prote	664	6	2.2	174	1	G69008	modulates DNA topo
591	6	2.2	119	2	S77748	probable ABC-type	665	6	2.2	174	2	C97964	hypothetical prote
592	6	2.2	119	2	A75586	hydrogenase expres	666	6	2.2	175	2	F69745	hypothetical prote
593	6	2.2	120	2	A84778	hypothetical prote	667	6	2.2	175	2	A64354	hypothetical prote
594	6	2.2	120	2	A84778	lipid transfer pro	668	6	2.2	175	2	E97553	hypothetical prote
595	6	2.2	122	2	T05950	probable membrane	669	6	2.2	176	2	S37737	hypothetical prote
596	6	2.2	123	2	B97181	hypothetical prote	670	6	2.2	176	2	I41076	hypothetical prote
597	6	2.2	124	2	A70692	probable membrane	671	6	2.2	177	2	H86710	probable kinase fr
598	6	2.2	124	2	S67606	carbomycin-resista	672	6	2.2	177	2	H97205	MHC class I histoc
599	6	2.2	124	2	JC1181	Ig heavy chain V r	673	6	2.2	178	2	C45831	hypothetical prote
600	6	2.2	125	2	S68170	hypothetical prote	674	6	2.2	178	2	D64036	hypothetical prote
601	6	2.2	126	2	S69804	translation initia	675	6	2.2	178	2	T03079	hypothetical prote
602	6	2.2	127	2	A75086	hypothetical prote	676	6	2.2	179	2	T30724	MHC class I histoc
603	6	2.2	129	2	H97938	blastocidin-S deam	677	6	2.2	180	2	D45831	suu ribosomal prot
604	6	2.2	130	2	S41571	hypothetical prote	678	6	2.2	180	2	C75171	ribosomal protein
605	6	2.2	130	2	B70818	hypothetical prote	679	6	2.2	180	2	D70161	hypothetical prote
606	6	2.2	131	2	E97737	hypothetical prote	680	6	2.2	181	2	S74491	adenylate kinase (
607	6	2.2	133	2	AI2834	conserved hypotet	681	6	2.2	181	2	F70105	ribonuclease H (rn
608	6	2.2	134	2	D97612	hypothetical 14.2K	682	6	2.2	181	2	D72468	hypothetical prote
609	6	2.2	135	2	D83795	transcription regu	683	6	2.2	181	2	T49759	related to microci
610	6	2.2	140	2	B81121	conserved hypotet	684	6	2.2	181	2	T35851	hypothetical prote
611	6	2.2	140	2	C64027	hypothetical prote	685	6	2.2	181	2	T35851	hypothetical prote
612	6	2.2	142	2	A32483	Ig heavy chain V r	686	6	2.2	181	2	AH2483	hypothetical prote
613	6	2.2	143	2	AC1322	hypothetical prote							

687	6	2.2	182	2	H71899	hypothetical prote	760	6	2.2	210	2	H83570	probable two-compo
688	6	2.2	183	2	AH1304	pyrimidine operon	761	6	2.2	210	2	AH0234	probable two-compo
689	6	2.2	183	2	AH1676	pyrimidine operon	762	6	2.2	210	2	T47033	hypothetical prote
690	6	2.2	183	2	AB3405	hypothetical prote	763	6	2.2	210	2	G95228	ABC transporter, A
691	6	2.2	184	2	AD1815	adenylate kinase (764	6	2.2	210	2	C98093	hypothetical prote
692	6	2.2	185	1	MOCH4E	myosin alkali ligh	765	6	2.2	212	2	G69369	branched-chain ami
693	6	2.2	185	2	S60778	dihydrodipicolinat	766	6	2.2	212	2	T03528	cob(I)alamin adeno
694	6	2.2	185	2	A70048	amino acid ABC tra	767	6	2.2	213	2	AF0408	adenyl-yl-sulfate k
695	6	2.2	185	2	AF2236	hypothetical prote	768	6	2.2	213	2	C64542	ABC transporter, A
696	6	2.2	186	2	S27735	hypothetical prote	769	6	2.2	213	2	C71965	ABC transporter, A
697	6	2.2	186	2	B72695	hypothetical prote	770	6	2.2	213	2	F97681	ABC-type transporter
698	6	2.2	186	2	T32408	hypothetical prote	771	6	2.2	213	2	AE2906	hypothetical prote
699	6	2.2	188	2	AB0132	conserved hypothet	772	6	2.2	213	2	F98019	hypothetical prote
700	6	2.2	188	2	AB3472	hypothetical prote	773	6	2.2	213	2	A95013	hypothetical prote
701	6	2.2	189	1	S74659	shikimate kinase (774	6	2.2	213	2	G95079	ABC transporter, A
702	6	2.2	189	2	A49558	hypothetical prote	775	6	2.2	213	2	T30618	hypothetical prote
703	6	2.2	190	2	JC0662	ribosomal protein	776	6	2.2	213	2	D97884	hypothetical prote
704	6	2.2	190	2	T03761	probable ribosomal	777	6	2.2	213	2	B97947	hypothetical prote
705	6	2.2	190	2	AD2386	hypothetical prote	778	6	2.2	214	1	S23663	hela protein - Rho
706	6	2.2	191	2	S51496	GTP-binding protei	779	6	2.2	214	2	A03309	dnak-type molecula
707	6	2.2	191	2	C64458	high-affinity bran	780	6	2.2	214	2	D86533	frame-shift with C
708	6	2.2	192	2	B68826	hypothetical prote	781	6	2.2	214	2	T14920	hypothetical prote
709	6	2.2	192	1	RSRT9	ribosomal protein	782	6	2.2	214	2	G72669	hypothetical prote
710	6	2.2	192	2	S65792	ribosomal protein	783	6	2.2	215	2	JC5483	ABC-type transporter
711	6	2.2	192	2	A84325	cytidylate kinase	784	6	2.2	215	2	C69767	conserved hypothet
712	6	2.2	192	2	AH0557	probable lipoprote	785	6	2.2	215	2	H90141	conserved hypothet
713	6	2.2	193	1	MOMS4E	myosin alkali ligh	786	6	2.2	215	2	B84078	hypothetical prote
714	6	2.2	193	1	MORT4E	myosin alkali ligh	787	6	2.2	216	2	B70317	H+-transporting tw
715	6	2.2	193	2	AF1323	3-isopropylmalate	788	6	2.2	216	2	H71892	osmoprotection ATP
716	6	2.2	193	2	AG1694	probable translati	789	6	2.2	216	2	C64622	osmoprotection pro
717	6	2.2	193	2	T14618	conserved hypothet	790	6	2.2	216	2	B82020	ABC transporter AT
718	6	2.2	193	2	C90469	conserved hypothet	791	6	2.2	216	2	T34527	hypothetical prote
719	6	2.2	194	1	MOCHLC	myosin alkali ligh	792	6	2.2	217	2	D81263	probable ABC trans
720	6	2.2	194	2	F69985	transcription regu	793	6	2.2	217	2	T33043	hypothetical prote
721	6	2.2	194	2	C98147	frck protein (AF19	794	6	2.2	218	2	C97236	ABC transporter, A
722	6	2.2	194	2	G71038	hypothetical prote	795	6	2.2	218	2	S76385	hypothetical prote
723	6	2.2	195	1	MOH03V	myosin alkali ligh	796	6	2.2	218	2	B80876	probable ABC-trans
724	6	2.2	195	2	A82416	conserved hypothet	797	6	2.2	218	2	H84644	PARA protein - Hel
725	6	2.2	195	2	T24033	hypothetical prote	798	6	2.2	218	2	AD2019	cell-division ATP-
726	6	2.2	197	1	MOH04E	myosin alkali ligh	799	6	2.2	218	2	G71197	hypothetical prote
727	6	2.2	197	2	E72294	thymidylate kinase	800	6	2.2	219	2	A70338	ABC transporter -
728	6	2.2	198	2	JQ0864	hypothetical 21.9K	801	6	2.2	219	2	AD1471	ABC transporters (
729	6	2.2	199	2	F81307	probable integral	802	6	2.2	219	2	AE3215	hypothetical prote
730	6	2.2	200	1	MORT3V	myosin alkali ligh	803	6	2.2	220	2	E75090	adenylate kinase (
731	6	2.2	200	2	E69912	adenylsulfate ki	804	6	2.2	220	2	G89192	ABC transporter (g
732	6	2.2	201	1	B65056	adenyl-yl-sulfate k	805	6	2.2	220	2	H71360	probable thiamin A
733	6	2.2	201	2	AH0856	adenosine 5'-phosp	806	6	2.2	220	2	H72252	cytidylate kinase
734	6	2.2	201	2	D91079	adenosine 5'-phosp	807	6	2.2	220	2	A13140	conserved hypothet
735	6	2.2	201	2	E85924	adenosine 5'-phosp	808	6	2.2	220	2	G90194	conserved hypothet
736	6	2.2	201	2	H82055	peptidyl-prolyl ci	809	6	2.2	220	2	G90047	hypothetical prote
737	6	2.2	202	1	S17244	adenyl-yl-sulfate k	810	6	2.2	220	2	AF1561	ABC transporter, A
738	6	2.2	202	2	T50101	adenylsulfate ki	811	6	2.2	220	2	AG1204	ABC transporter, A
739	6	2.2	202	2	B83836	adenylsulfate ki	812	6	2.2	220	2	F71052	probable adenylate
740	6	2.2	202	2	B90180	ABC transporter, A	813	6	2.2	221	2	G81335	probable ABC trans
741	6	2.2	203	2	E83166	hypothetical prote	814	6	2.2	221	2	AF1862	ATP-binding protei
742	6	2.2	204	2	D95394	probable transcrip	815	6	2.2	221	2	B84160	amino acid ABC tra
743	6	2.2	205	2	T10296	fibroblast growth	816	6	2.2	221	2	F69369	branched-chain ami
744	6	2.2	205	2	F87660	hydrolase, haloaci	817	6	2.2	221	2	E78834	ABC transporter AT
745	6	2.2	205	2	T04918	hypothetical prote	818	6	2.2	221	2	F71676	glutamine transpor
746	6	2.2	206	2	A84236	30S ribosomal prot	819	6	2.2	222	2	AD1137	ribulose-5-phospha
747	6	2.2	206	2	AC0520	conserved hypothet	820	6	2.2	222	2	AC1495	hypothetical prote
748	6	2.2	206	2	C85493	probable DNA repai	821	6	2.2	222	2	AF3133	H+-exporting ATPas
749	6	2.2	206	2	G90642	probable DNA repai	822	6	2.2	222	2	C25014	hypothetical prote
750	6	2.2	206	2	G64732	yacE protein - Esc	823	6	2.2	222	2	C96992	hypothetical prote
751	6	2.2	206	2	AH0416	conserved hypothet	824	6	2.2	222	2	T34753	probable ATP/GTP b
752	6	2.2	206	2	A95331	probable cytochrom	825	6	2.2	222	2	AE0182	ABC transporter AT
753	6	2.2	207	2	T21903	hypothetical prote	826	6	2.2	223	2	D64613	cell division prot
754	6	2.2	207	2	F75535	deoxyguanosine kin	827	6	2.2	223	2	E71900	probable ABC trans
755	6	2.2	207	2	A10002	secreted thiol,dis	828	6	2.2	223	2	E83596	DNA mismatch repai
756	6	2.2	207	2	G95864	probable ABC trans	829	6	2.2	223	2	C86707	ABC transporter AT
757	6	2.2	207	2	B82480	transcription regu	830	6	2.2	223	2	H86906	ABC transporter AT
758	6	2.2	208	2	B44261	dnak-type molecula	831	6	2.2	223	2	D83869	ABC transporter (A
759	6	2.2	209	2	T29196	hypothetical prote	832	6	2.2	223	2	B83697	hypothetical prote

833	2.2	6	2.2	223	2	B97178	ABC transporter, A	906	6	2.2	231	2	C69317	conserved hypothet
834	2.2	6	2.2	223	2	S74812	ABC-type transporter	907	6	2.2	231	2	B86154	T6A9.7 protein - A
835	2.2	6	2.2	224	2	AC1485	ABC transporter, A	908	6	2.2	231	2	C70000	ABC transporter (A
836	2.2	6	2.2	224	2	C82903	cytidylate kinase	909	6	2.2	231	2	C81909	probable ABC-trans
837	2.2	6	2.2	224	2	T43331	clathrin light cha	910	6	2.2	232	2	B83922	ABC transporter, A
838	2.2	6	2.2	224	2	T72346	basal-body rod mod	911	6	2.2	232	2	B84728	probable ABC-type
839	2.2	6	2.2	224	2	T72046	conserved hypothet	912	6	2.2	232	2	F85488	hypothetical prote
840	2.2	6	2.2	224	2	A86579	CT668 hypothetical	913	6	2.2	232	2	F90637	hypothetical prote
841	2.2	6	2.2	224	2	B97146	ABC-type transporter	914	6	2.2	232	2	A11946	hypothetical prote
842	2.2	6	2.2	224	2	B70327	ABC transporter -	915	6	2.2	232	2	G84382	cobalt transporter A
843	2.2	6	2.2	225	2	A36459	orotate phosphorib	916	6	2.2	232	2	C97089	ABC transporter, A
844	2.2	6	2.2	225	2	E90260	ABC transporter, A	917	6	2.2	232	2	C69822	ABC transporter, A
845	2.2	6	2.2	225	2	B91104	probable ABC trans	918	6	2.2	232	2	C69822	glycine betaine/L-
846	2.2	6	2.2	225	2	B85949	probable ABC trans	919	6	2.2	233	2	B90210	hypothetical prote
847	2.2	6	2.2	225	2	AH1294	hypothetical prote	920	6	2.2	233	2	D96763	hypothetical prote
848	2.2	6	2.2	225	2	F71439	probable serine pr	921	6	2.2	233	2	B95091	ABC transporter, A
849	2.2	6	2.2	225	2	F89795	hypothetical prote	922	6	2.2	233	2	C97358	hypothetical prote
850	2.2	6	2.2	225	2	AB2374	ABC transporter AT	923	6	2.2	233	2	A77337	ABC-type transporter
851	2.2	6	2.2	226	2	D69433	ABC transporter, A	924	6	2.2	233	2	A82184	ABC transporter, A
852	2.2	6	2.2	226	2	S75665	ABC-type transporter	925	6	2.2	233	2	AF1994	ATP-binding protei
853	2.2	6	2.2	226	2	B75270	ABC transporter, A	926	6	2.2	233	2	JQ0097	hypothetical 26K p
854	2.2	6	2.2	226	2	A97340	ABC-type nucleoti	927	6	2.2	233	2	D96763	hypothetical prote
855	2.2	6	2.2	226	2	D35719	hisp-like nucleoti	928	6	2.2	233	2	D97118	RNA polymerase sig
856	2.2	6	2.2	226	2	D86104	ATP-binding compon	929	6	2.2	233	2	AC0645	ABC transporter AT
857	2.2	6	2.2	226	2	G91263	ATP-binding compon	930	6	2.2	234	2	H72385	ABC transporter, A
858	2.2	6	2.2	226	2	S60562	H+-transporting tw	931	6	2.2	234	2	T37141	probable membrane
859	2.2	6	2.2	226	2	A31335	H+-exporting ATPas	932	6	2.2	234	2	A70736	hypothetical prote
860	2.2	6	2.2	226	2	T34827	probable potassium	933	6	2.2	234	2	H87364	ABC transporter, A
861	2.2	6	2.2	226	2	A12774	ribose 5-phosphate	934	6	2.2	234	2	H69253	conserved hypothet
862	2.2	6	2.2	226	2	B89782	hypothetical prote	935	6	2.2	234	2	D96932	ABC transporter, A
863	2.2	6	2.2	226	2	AB1741	ABC transporter AT	936	6	2.2	234	2	AF0198	lipoprotein releas
864	2.2	6	2.2	226	2	AD1371	ABC-transporter AT	937	6	2.2	234	2	AC1094	high-affinity zinc
865	2.2	6	2.2	227	2	C71307	probable ABC trans	938	6	2.2	234	2	A11456	high-affinity zinc
866	2.2	6	2.2	227	2	A75304	ABC transporter, A	939	6	2.2	235	1	B63350	25K protein - whit
867	2.2	6	2.2	227	2	B84040	ABC transporter (A	940	6	2.2	235	2	AB2613	monop
868	2.2	6	2.2	227	2	A84109	ABC transporter (A	941	6	2.2	235	2	I68700	MHC HLA-A cell sur
869	2.2	6	2.2	227	2	A64129	probable ABC-type	942	6	2.2	235	2	S60887	ferric exochelin u
870	2.2	6	2.2	227	2	AI0875	probable ABC-trans	943	6	2.2	235	2	AG0515	hypothetical ABC t
871	2.2	6	2.2	227	2	B83288	probable ATP-bind	944	6	2.2	235	2	D64399	glutamine transpor
872	2.2	6	2.2	227	2	D83271	probable ATP-bind	945	6	2.2	235	2	G71259	probable ABC trans
873	2.2	6	2.2	227	2	B82177	ABC transporter, A	946	6	2.2	235	2	D90790	probable ATP bindi
874	2.2	6	2.2	227	2	B82408	ABC transporter, A	947	6	2.2	235	2	G85650	probable ATP bindi
875	2.2	6	2.2	227	2	F96955	ABC transporter, A	948	6	2.2	235	2	T50170	hypothetical prote
876	2.2	6	2.2	227	2	F96364	ABC transporter, A	949	6	2.2	235	2	H96023	probable phosphon
877	2.2	6	2.2	228	2	AF0565	hypothetical ABC t	950	6	2.2	235	2	S69697	hypothetical prote
878	2.2	6	2.2	228	2	A96939	ABC transporter, A	951	6	2.2	235	2	AB2598	hypothetical prote
879	2.2	6	2.2	228	2	B69377	ABC transporter AT	952	6	2.2	235	2	G86519	ABC transport ATPa
880	2.2	6	2.2	228	2	F90698	probable ABC-type	953	6	2.2	235	2	D72102	ABC transporter, A
881	2.2	6	2.2	228	2	F64780	probable ABC-type	954	6	2.2	236	2	B72369	ABC transporter, A
882	2.2	6	2.2	228	2	H85548	probable ABC-trans	955	6	2.2	236	2	T07260	sulfate transport
883	2.2	6	2.2	228	2	AF0374	probable ABC trans	956	6	2.2	236	2	D69423	branched-chain ami
884	2.2	6	2.2	228	2	D83071	probable ATP-bind	957	6	2.2	236	2	D90461	hypothetical prote
885	2.2	6	2.2	228	2	T37623	hypothetical prote	958	6	2.2	236	2	I39835	transcription acti
886	2.2	6	2.2	228	2	B64856	probable ABC-type	959	6	2.2	236	2	D84103	two-component resp
887	2.2	6	2.2	228	2	A75516	ABC transporter, A	960	6	2.2	236	2	S01086	hypothetical prote
888	2.2	6	2.2	228	2	G90815	hypothetical prote	961	6	2.2	236	2	AG2905	hypothetical prote
889	2.2	6	2.2	228	2	C85675	hypothetical prote	962	6	2.2	236	2	H97680	probable ATP-bind
890	2.2	6	2.2	228	2	AB2147	ABC transporter, A	963	6	2.2	236	2	F82934	ABC transporter UU
891	2.2	6	2.2	229	2	T45311	cell division atp-	964	6	2.2	236	2	C71517	probable ABC trans
892	2.2	6	2.2	229	2	E70919	cell division atp-	965	6	2.2	237	2	AF2196	heme oxygenase [im
893	2.2	6	2.2	229	2	E96558	hypothetical prote	966	6	2.2	237	2	F86789	manganese ABC tran
894	2.2	6	2.2	229	2	T40789	clathrin light cha	967	6	2.2	237	2	G65084	hypothetical prote
895	2.2	6	2.2	229	2	F70405	probable ABC-type	968	6	2.2	237	2	C83689	hypothetical prote
896	2.2	6	2.2	229	2	E70405	ABC transporter -	969	6	2.2	238	2	I68699	MHC HLA-A cell sur
897	2.2	6	2.2	230	2	T28262	ORF MSV100 probabl	970	6	2.2	238	2	AF0607	arginine transport
898	2.2	6	2.2	230	2	AC1059	ABC transporter, A	971	6	2.2	238	2	F64824	arginine 3rd trans
899	2.2	6	2.2	230	2	AB1462	ABC transporter, A	972	6	2.2	238	2	B85597	arginine 3rd trans
900	2.2	6	2.2	230	2	H65084	hypothetical prote	973	6	2.2	238	2	A90747	arginine 3rd trans
901	2.2	6	2.2	230	2	H97343	ABC transport syst	974	6	2.2	238	2	AH0164	cobalt transport A
902	2.2	6	2.2	230	2	F83697	ABC transporter (A	975	6	2.2	238	2	H69479	probable glutamine
903	2.2	6	2.2	230	2	C71548	probable ABC trans	976	6	2.2	238	2	C72576	probable ATP-bind
904	2.2	6	2.2	231	2	C81107	ABC transporter, A	977	6	2.2	238	2	A83224	
905	2.2	6	2.2	231	2	G97554	ribose 5-phosphate	978	6	2.2	238	2		

979 6 2.2 238 2 AG2909 hypothetical prote
980 6 2.2 238 2 E71375 probable ABC trans
981 6 2.2 238 2 F75035 iron (iii) abc tra
982 6 2.2 239 2 H97578 ABC transporter, A
983 6 2.2 239 2 A92799 hypothetical prote
984 6 2.2 239 2 F82386 amino acid ABC tra
985 6 2.2 239 2 AG0420 phosphonates trans
986 6 2.2 239 2 E70800 probable transport
987 6 2.2 239 2 S64324 probable membrane
988 6 2.2 239 2 AE1317 hypothetical prote
989 6 2.2 240 1 QRECGQ glutamine transpor
990 6 2.2 240 2 A35448 small nuclear ribo
991 6 2.2 240 2 A10600 glutamine transport
992 6 2.2 240 2 H69962 ABC-type transporter
993 6 2.2 240 2 G83832 ABC transporter (A
994 6 2.2 240 2 G90739 hypothetical prote
995 6 2.2 240 2 A85590 hypothetical prote
996 6 2.2 240 2 D97762 probable ABC trans
997 6 2.2 240 2 AC0307 probable glutamine
998 6 2.2 240 2 S20860 regulatory protein
999 6 2.2 240 2 Q98277 hypothetical prote
1000 6 2.2 240 2 AC3007 hypothetical prote

ALIGNMENTS

RESULT 1
C95259
ABC transporter, ATP-binding protein SP2220 [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 16-Aug-2004
C:Accession: C95259
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
non, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95259
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-279 <KUR>
A:Cross-references: UNIPROT:Q97N51; GB:AE005672; PIDN:AAK76268.1; PID:g14973730; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2220
C:Superfamily: ATP-binding cassette homology

Query Match 100.0%; Score 279; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 3.5e-271;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIALENVFTYQEGTPLASALSVDLSLTIEDGYSYALIGHTGSGKSTIQLLGLLVPS 60
DB 1 MGIALENVFTYQEGTPLASALSVDLSLTIEDGYSYALIGHTGSGKSTIQLLGLLVPS 60
QY 61 QGSVRVFDLTITSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGPNQFVSEED 120
DB 61 QGSVRVFDLTITSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGPNQFVSEED 120
QY 121 AVKTAREKALVGIDESLFDSPFELSGQGMRRVAIAGILAMEPAIVLDEPTAGLDPLG 180
DB 121 AVKTAREKALVGIDESLFDSPFELSGQGMRRVAIAGILAMEPAIVLDEPTAGLDPLG 180
QY 181 RKELMTLTKHQSGMTIIVLTHLMDDDVAEYANQYVMEKGRVLKGGKPSDVFDQVFM 240
DB 181 RKELMTLTKHQSGMTIIVLTHLMDDDVAEYANQYVMEKGRVLKGGKPSDVFDQVFM 240
QY 241 EYQLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESLNG 279
DB 241 EYQLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESLNG 279

RESULT 2

F98124
hypothetical protein ABC-NBP [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 16-Aug-2004
C:Accession: F98124
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: F98124
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-279 <KUR>
A:Cross-references: UNIPROT:Q8DMY0; GB:AE007317; PIDN:AAI00827.1; PID:g15459731; GSPDB:G
C:Genetics:
A:Gene: ABC-NBP
C:Superfamily: ATP-binding cassette homology

Query Match 59.9%; Score 167; DB 2; Length 279;
Best Local Similarity 99.6%; Pred. No. 4.9e-159;
Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 YQEGTPLASALSVDLSLTIEDGYSYALIGHTGSGKSTIQLLGLLVPSQGSVRVFDTLI 71
DB 12 YQEGTPLASALSVDLSLTIEDGYSYALIGHTGSGKSTIQLLGLLVPSQGSVRVFDTLI 71
QY 72 TSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGPNQFVSEEDAVKTAREKAL 131
DB 72 TSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGPNQFVSEEDAVKTAREKAL 131
QY 132 VGIDESLFDSPFELSGQGMRRVAIAGILAMEPAIVLDEPTAGLDPLGRKELMTLPK 191
DB 132 VGIDESLFDSPFELSGQGMRRVAIAGILAMEPAIVLDEPTAGLDPLGRKELMTLPK 191
QY 192 HQSGMTIIVLTHLMDDDVAEYANQYVMEKGRVLKGGKPSDVFDQVFMERYQLGVPKITA 251
DB 192 HQSGMTIIVLTHLMDDDVAEYANQYVMEKGRVLKGGKPSDVFDQVFMERYQLGVPKITA 251
QY 252 FCKRLADRGVSFKRLPIKIEEFKESLNG 279
DB 252 FCKRLADRGVSFKRLPIKIEEFKESLNG 279

RESULT 3

F86659
ABC transporter ATP-binding protein ychB [imported] - Lactococcus lactis subsp. lactis (C
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 16-Aug-2004
C:Accession: F86659
R:Solotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86659
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <STO>
A:Cross-references: UNIPROT:Q9CIS8; GB:AE005176; PID:g12723140; PIDN:AAK04376.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: ychB
C:Superfamily: ATP-binding cassette homology

Query Match 8.2%; Score 23; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 7.9e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 SPFELSGGQRRVAIAGILAMEP 164
|||||
Db 141 SPFELSGGQRRVAIAGILAMEP 163

RESULT 4
E69742
ABC transporter (ATP-binding protein) homolog ybaE - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E69742
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-276 <KUN>
A;Cross-references: UNIPROT:P70970; GB:Z39104; GB:AL009126; NID:g2632267; PIDN:CAB11922.
A;Experimental source: strain 168
C/Genetics:
C;Gene: ybaE
C;Superfamily: ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;10-209/Domain: ATP-binding cassette homology <ABC>
F;27-34/Region: nucleotide-binding motif A (P-loop)

Query Match 6.8%; Score 19; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 7.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 DRSPFELSGGQRRVAIAG 158
|||||
Db 127 DRSPFELSGGQRRVAIAG 145

RESULT 5
AH1399
ABC transporter (ATP-binding protein) homolog lmo2600 [imported] - Listeria monocytogenes
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AH1399
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blocker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Feihl, H.
Science 294, 849-852, 2001
A;Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simeos, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1399
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-288 <GLA>
A;Cross-references: UNIPROT:O8Y455; GB:NC_003210; PIDN:CAD00678.1; PID:g16412088; GSPDB
A;Experimental source: strain EGD-e
C/Genetics:
A;Gene: lmo2600
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
C:Accession: B83670
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; PMID:11058132
A:Accession: B83670
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <STO>
A:Cross-references: UNIPROT:Q9KGD6; GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BA8038
A:Experimental source: strain C-125
C:Genetics:
C:Superfamily: ATP-binding cassette homology

Query Match 4.7%; Score 13; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 LSGGQRRVAIAG 158
|||||
DB 134 LSGGQRRVAIAG 146
|||||

RESULT 9
C90560
ABC transporter atp-binding protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004
C:Accession: C90560
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A95512; PMID:11353084
A:Accession: C90560
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <KUR>
A:Cross-references: UNIPROT:Q9OH4; GB:AL445566; PID:g14089801; PIDN:CAC13560.1; GSPDB:G
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU 3870
A:Genetic code: SGC3
C:Superfamily: ATP-binding cassette homology

Query Match 4.3%; Score 12; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LVLDPTAGLDLP 178
|||||
DB 183 LVLDPTAGLDLP 194
|||||

RESULT 10
G72598
probable ABC transporter ATP-binding protein APE1255 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 16-Aug-2004
C:Accession: G72598
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; PMID:99310339; PMID:10382966
A:Accession: G72598
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <RAW>
A:Cross-references: UNIPROT:Q9YCK2; DDBJ:AP000061; NID:g5104821; PIDN:BA80245.1; PID:dl
A:Experimental source: strain K1

C:Genetics:
A:Gene: APE1255
C:Superfamily: ATP-binding cassette homology

Query Match 3.9%; Score 11; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLDEPTAGLDLP 178
|||||
DB 164 VLDEPTAGLDLP 174
|||||

RESULT 11
G64435
cobalt transport ATP-binding protein O homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C:Accession: G64435
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.
; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
reon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A:Reference number: A64300; PMID:96337999; PMID:8688087
A:Accession: G64435
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-279 <BUL>
A:Cross-references: UNIPROT:Q58488; GB:U67551; GB:L77117; NID:g1591728; PIDN:AAB99089.1;
C:Genetics:
A:Map position: REV1027976-1027137
C:Superfamily: ATP-binding cassette homology
C:Keywords: ATP; nucleotide binding; P-loop
F:20-215/Domain: ATP-binding cassette homology <ABC>
F:37-44/Region: nucleotide-binding motif A (P-loop)

Query Match 3.9%; Score 11; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLDEPTAGLDLP 178
|||||
DB 162 VLDEPTAGLDLP 172
|||||

RESULT 12
S34187
probable ABC-type transport protein TnrB2 - Streptomyces longisporoflavus
C:Species: Streptomyces longisporoflavus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-2004
C:Accession: S34187; S42415
R:Cooper, H.N.
submitted to the EMBL Data Library, June 1993
A:Reference number: S34187
A:Accession: S34187
A:Molecule type: DNA
A:Residues: 1-300 <COO>
A:Cross-references: UNIPROT:Q54406; EMBL:X73633; NID:g313336; PIDN:CAAS2012.1; PID:g5817
R:Linton, K.J.; Cooper, H.N.; Hunter, I.S.; Leadlay, P.F.
Mol. Microbiol. 11, 777-785, 1994
A:Title: An ABC-transporter from Streptomyces longisporoflavus confers resistance to the
A:Reference number: S42415; PMID:94254733; PMID:8196549
A:Accession: S42415
A:Molecule type: DNA
A:Residues: 14-53;123-162 <LIN>
A:Cross-references: EMBL:X73633
A:Experimental source: strain 83E6
C:Genetics:
A:Start codon: GTG
C:Superfamily: ATP-binding cassette homology
C:Keywords: antibiotic resistance; ATP; nucleotide binding; P-loop

F:14-200/Domain: ATP-binding cassette homology <ABC>
F:31-38/Region: nucleotide-binding motif A (P-loop)

Query Match 3.6%; Score 11; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDPL 179
Db 148 LDEPTAGLDPL 158
|||||

RESULT 13

S77760
Probable ABC-type transport protein - Mycoplasma capricolum (fragment)
N:Alternate names: protein MC453
C:Species: Mycoplasma capricolum
C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 16-Aug-2004
C:Accession: S77760
R:Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.;
Mol. Microbiol. 16, 955-967, 1995
A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology
A:Reference number: S77739; MUID:96059641; PMID:7476192
A:Accession: S77760
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-178 <SOR>
A:Cross-references: UNIPROT:Q49088; EMBL:Z33339; NID:G559469; PIDN:CAA83843.1; PID:G5604
A:Experimental source: ATCC 27343
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: ATP-binding cassette homology
C:Keywords: ATP
F:1-153/Domain: ATP-binding cassette homology (fragment) <ABCX>

Query Match 3.6%; Score 10; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQ 150
Db 72 RSPFELSGGQ 81
|||||

RESULT 14

G83245
Probable ATP-binding component of ABC transporter PA3212 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: G83245
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brinkman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83245
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STO>
A:Cross-references: UNIPROT:Q9HZ28; GB:AE004744; GB:AE004091; NID:G9949317; PIDN:AAG0660
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3212

Query Match 3.6%; Score 10; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDLP 178
Db 170 LDEPTAGLDLP 179
|||||

RESULT 15

AG1225
cobalt transport ATP-binding protein ChlO homolog lmo1207 [imported] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG1225
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Anand, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1225
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <GLA>
A:Cross-references: UNIPROT:Q8Y7R4; GB:NC_003210; PIDN:CAC99285.1; PID:G16410623; GSPDB:(
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1207

Query Match 3.6%; Score 10; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDLP 178
Db 161 LDEPTAGLDLP 170
|||||

Search completed: October 28, 2005, 18:16:32
Job time : 59 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 18:02:13 ; Search time 175 Seconds

(without alignments)
816.401 Million cell updates/sec

Title: US-09-769-744d-26

Perfect score: 279

Sequence: 1 MGIALENVNTYQETPLAS.....GVSEKRLPIKIEPKESLNG 279

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	279	100.0	279	Q97N51	Q97N51 streptococ
2	167	59.9	279	Q8DMY0	Q8DMY0 streptococ
3	23	8.2	288	Q9CIS8	Q9CIS8 lactococcus
4	22	7.9	280	Q99X12	Q99X12 streptococ
5	22	7.9	280	Q7CMM8	Q7CMM8 streptococ
6	22	7.9	280	Q8DRS0	Q8DRS0 streptococ
7	22	7.9	280	Q8DMR4	Q8DMR4 streptococ
8	22	7.9	280	Q8E2L3	Q8E2L3 streptococ
9	22	7.9	280	Q8KSH2	Q8KSH2 streptococ
10	19	6.8	276	P70970	P70970 bacillus su
11	19	6.8	289	Q65P76	Q65P76 bacillus li
12	18	6.5	177	Q8VNL8	Q8VNL8 enterococcu
13	18	6.5	288	Q8Y455	Q8Y455 listeria mo
14	18	6.5	288	Q927N9	Q927N9 listeria in
15	18	6.5	288	Q71WH8	Q71WH8 listeria mo
16	18	6.5	293	Q63H61	Q63H61 bacillus ce
17	18	6.5	293	Q73F66	Q73F66 bacillus ce
18	18	6.5	293	Q81J15	Q81J15 bacillus ce
19	18	6.5	293	Q81VQ1	Q81VQ1 bacillus th
20	18	6.5	293	Q6HPM9	Q6HPM9 bacillus th
21	17	6.1	289	Q74L61	Q74L61 lactobacill
22	17	6.1	291	Q839D4	Q839D4 enterococcu
23	16	5.7	295	Q88XV1	Q88XV1 lactobacill
24	13	4.7	183	Q29J22	Q29J22 bacillus ha
25	13	4.7	282	Q9KG06	Q9KG06 bacillus ha
26	12	4.3	285	Q8XW33	Q8XW33 clostridium
27	12	4.3	288	Q890R3	Q890R3 clostridium
28	12	4.3	289	Q8ETV6	Q8ETV6 oceanobacil
29	12	4.3	297	Q51719	Q51719 propionibac
30	12	4.3	304	Q98QH4	Q98QH4 mycoplasma
31	12	4.3	305	Q6XYZ3	Q6XYZ3 Spiroplasma

32	12	4.3	326	2	Q8TIX0	Q8TIX0 methanosarc
33	12	4.3	327	2	Q8PYH5	Q8PYH5 methanosarc
34	11	3.9	253	2	Q9YCK2	Q9YCK2 aeropyrum p
35	11	3.9	279	1	CEIO_METUA	CEIO_METUA methanococ
36	11	3.9	279	2	Q7W0L5	Q7W0L5 bordetella
37	11	3.9	279	2	Q7W230	Q7W230 bordetella
38	11	3.9	279	2	Q7WR08	Q7WR08 bordetella
39	11	3.9	286	2	Q8R7Y5	Q8R7Y5 thermosanaer
40	11	3.9	300	2	Q54406	Q54406 streptomyc
41	11	3.9	483	2	Q8N2S4	Q8N2S4 homo sapien
42	11	3.9	546	2	Q6ABD5	Q6ABD5 propionibac
43	11	3.9	573	2	Q74DV0	Q74DV0 geobacter s
44	11	3.9	601	2	Q8ZG45	Q8ZG45 streptomyc
45	11	3.9	856	2	Q9GMD8	Q9GMD8 homo sapien
46	11	3.9	1129	2	Q6AI35	Q6AI35 homo sapien
47	11	3.9	1623	2	Q8K449	Q8K449 mus musculu
48	11	3.9	1624	2	Q8IUA7	Q8IUA7 homo sapien
49	11	3.9	1624	2	Q8WWZ5	Q8WWZ5 homo sapien
50	10	3.6	77	2	Q71J33	Q71J33 lactobacill
51	10	3.6	178	2	Q49088	Q49088 mycoplasma
52	10	3.6	259	2	Q82XY5	Q82XY5 nitrosomona
53	10	3.6	263	2	Q88RI8	Q88RI8 pseudomonas
54	10	3.6	264	2	Q9HZ28	Q9HZ28 pseudomonas
55	10	3.6	268	2	Q8Y7R4	Q8Y7R4 listeria mo
56	10	3.6	268	2	Q92CK1	Q92CK1 listeria in
57	10	3.6	268	2	Q720M2	Q720M2 listeria mo
58	10	3.6	271	1	CBIO_SALTY	CBIO_SALTY salmonella
59	10	3.6	271	2	Q825N5	Q825N5 salmonella
60	10	3.6	272	2	Q62N03	Q62N03 burkholderi
61	10	3.6	275	2	Q72EG7	Q72EG7 desulfovibr
62	10	3.6	276	2	Q8TIW9	Q8TIW9 methanosarc
63	10	3.6	276	2	Q8PCS8	Q8PCS8 xanthomonas
64	10	3.6	277	2	Q50801	Q50801 methanobact
65	10	3.6	277	2	Q82QH7	Q82QH7 streptomyc
66	10	3.6	278	2	Q6AAN0	Q6AAN0 propionibac
67	10	3.6	278	2	Q9A5X8	Q9A5X8 caulobacter
68	10	3.6	279	2	Q87DX6	Q87DX6 xylella fas
69	10	3.6	280	2	Q63XY7	Q63XY7 burkholderi
70	10	3.6	280	2	Q8PGP5	Q8PGP5 xanthomonas
71	10	3.6	284	2	Q54187	Q54187 streptomyc
72	10	3.6	285	2	Q8XNY7	Q8XNY7 clostridium
73	10	3.6	286	2	Q97EK9	Q97EK9 clostridium
74	10	3.6	286	2	Q8CR17	Q8CR17 staphylococ
75	10	3.6	286	2	Q9PDS7	Q9PDS7 xylella fas
76	10	3.6	288	2	Q67JX4	Q67JX4 symbiobacte
77	10	3.6	289	2	Q8KFD6	Q8KFD6 chlorobium
78	10	3.6	292	2	Q8NNX0	Q8NNX0 corynebacte
79	10	3.6	298	2	Q8Y2M1	Q8Y2M1 ralstonia s
80	10	3.6	299	2	Q6AB92	Q6AB92 propionibac
81	10	3.6	302	2	Q8EPV0	Q8EPV0 shewanella
82	10	3.6	303	1	Y180_MYCPN	Y180_MYCPN mycoplasma
83	10	3.6	303	2	Q6MSQ2	Q6MSQ2 mycoplasma
84	10	3.6	304	1	Y180_MYCGE	Y180_MYCGE mycoplasma
85	10	3.6	307	2	Q9XAC8	Q9XAC8 streptomyc
86	10	3.6	308	2	Q6KHL2	Q6KHL2 mycoplasma
87	10	3.6	310	2	Q829T7	Q829T7 streptomyc
88	10	3.6	311	2	Q27739	Q27739 methanobact
89	10	3.6	315	2	Q6FLW4	Q6FLW4 mesoplasma
90	10	3.6	318	2	Q7NAQ7	Q7NAQ7 mycoplasma
91	10	3.6	406	2	Q8EUF2	Q8EUF2 mycoplasma
92	10	3.6	433	2	Q9PPV2	Q9PPV2 ureaplasma
93	10	3.6	549	2	Q733M4	Q733M4 bacillus ce
94	10	3.6	549	2	Q81Y81	Q81Y81 bacillus an
95	10	3.6	564	2	Q6HVF5	Q6HVF5 bacillus th
96	10	3.6	572	2	Q81AA2	Q81AA2 bacillus ce
97	10	3.6	587	2	Q637E9	Q637E9 bacillus ce
98	10	3.6	587	2	Q733E4	Q733E4 bacillus ce
99	10	3.6	587	2	Q81Y19	Q81Y19 bacillus an
100	10	3.6	587	2	Q6HFC3	Q6HFC3 bacillus th
101	10	3.6	601	2	Q9KDT5	Q9KDT5 bacillus ha
102	10	3.6	610	2	Q8ERA0	Q8ERA0 oceanobacil
103	10	3.6	888	2	Q7RBT4	Q7RBT4 plasmodium
104	10	3.6				

105	10	3.6	1543	2	Q8WVZ4	Q8WVZ4 homo sapien	178	9	3.2	500	2	Q8U7X8	Q8u7x8 agrobacteri
106	10	3.6	1543	2	Q7Z219	Q7Z219 homo sapien	179	9	3.2	503	2	Q8AB11	Q8ab11 bacteroides
107	10	3.6	1574	2	Q69ZY4	Q69ZY4 mus musculus	180	9	3.2	505	2	Q9CL10	Q9cl10 pasteurella
108	10	3.6	1591	2	Q94911	Q94911 homo sapien	181	9	3.2	508	2	Q92XH3	Q92xh3 rhizobium m
109	10	3.6	1620	2	Q8K440	Q8K440 mus musculus	182	9	3.2	528	2	Q82BT2	Q82bt2 streptomyce
110	10	3.6	1620	2	Q8K442	Q8K442 mus musculus	183	9	3.2	545	2	Q637L3	Q637l3 bacillus ce
111	9	3.2	126	2	Q84TX9	Q84jx9 arabidopsis	184	9	3.2	554	2	Q67511	Q67511 aquifex aeo
112	9	3.2	126	2	Q84VL1	Q84v11 arabidopsis	185	9	3.2	559	2	Q7W090	Q7w090 bordetella
113	9	3.2	168	2	Q899Y3	Q899y3 clostridium	186	9	3.2	559	2	Q7W311	Q7w311 bordetella
114	9	3.2	194	2	Q8DM53	Q8dm53 synchococc	187	9	3.2	565	2	Q9CIN1	Q9cin1 lactococcus
115	9	3.2	201	1	CCMA_RHILO	Q98ea4 rhizobium l	188	9	3.2	566	2	Q7WEY6	Q7wey6 bordetella
116	9	3.2	209	2	Q7VBR6	Q7vbr6 prochloroco	189	9	3.2	579	2	Q7P0D7	Q7p0d7 chromobacte
117	9	3.2	210	2	Q55649	Q55649 synchococyt	190	9	3.2	580	1	MDLB_BUCAI	P57552 buchnera ap
118	9	3.2	210	2	Q7V7F8	Q7v7f8 prochloroco	191	9	3.2	591	2	Q7MJW4	Q7mjw4 vibrio vuln
119	9	3.2	214	2	Q7U732	Q7u732 synchococcc	192	9	3.2	591	2	Q8DAA9	Q8daa9 vibrio vuln
120	9	3.2	215	2	Q7V225	Q7v225 prochloroco	193	9	3.2	591	2	Q6D816	Q6d816 erwinia car
121	9	3.2	215	2	Q8DJC9	Q8djcc synchococcc	194	9	3.2	592	2	Q6LTJ3	Q6ltj3 photobacter
122	9	3.2	224	2	Q8YMQ7	Q8yqg7 anabaena sp	195	9	3.2	592	2	Q87PS0	Q87ps0 vibrio para
123	9	3.2	242	2	Q9HPH7	Q9hph7 halobacteri	196	9	3.2	593	1	MDLB_ECOLI	P75706 escherichia
124	9	3.2	244	2	Q8KFK0	Q8kfk0 chlorobium	197	9	3.2	593	2	Q828U4	Q828u4 salmonella
125	9	3.2	246	2	Q67R20	Q67r20 symbiobacte	198	9	3.2	593	2	Q8ZRB3	Q8zrb3 salmonella
126	9	3.2	247	2	Q7V4Q8	Q7v4q8 prochloroco	199	9	3.2	594	2	Q7UD14	Q7udi4 shigella fl
127	9	3.2	248	2	Q6MHX2	Q6mhx2 bdellovibri	200	9	3.2	594	2	Q7N0M4	Q7n0m4 photorhabdu
128	9	3.2	248	2	Q822Q2	Q822q2 chlamydophi	201	9	3.2	605	2	P72607	P72607 synchococyt
129	9	3.2	251	2	Q7U9P2	Q7u9p2 synchococcc	202	9	3.2	607	2	Q66DS1	Q66ds1 yersinia ps
130	9	3.2	256	2	Q74HR9	Q74hr9 lactobacill	203	9	3.2	607	2	Q8ZC78	Q8zc78 yersinia pe
131	9	3.2	260	2	P72734	P72734 synchococyt	204	9	3.2	611	2	Q9CIU5	Q9cius lactococcus
132	9	3.2	260	2	P73030	P73030 synchococyt	205	9	3.2	616	2	Q8D152	Q8d152 yersinia pe
133	9	3.2	260	2	Q820B8	Q820b8 anabaena sp	206	9	3.2	631	2	Q83M47	Q83m47 shigella fl
134	9	3.2	262	2	Q7NDM8	Q7ndw8 gloebacter	207	9	3.2	646	2	Q6MCG4	Q6mcg4 parachlamyd
135	9	3.2	267	2	Q7UXL9	Q7uxl9 rhodopirell	208	9	3.2	697	1	YN26_MYCTU	P63399 mycobacteri
136	9	3.2	268	2	Q8DLZ8	Q8dlz8 synchococcc	209	9	3.2	697	1	YN53_MYCBO	P63400 mycobacteri
137	9	3.2	270	2	Q7VDP7	Q7vdp7 prochloroco	210	9	3.2	714	2	Q73Y59	Q73y59 mycobacteri
138	9	3.2	271	2	Q7P788	Q7p788 fusobacteri	211	9	3.2	724	2	Q9CCF9	Q9ccf9 mycobacteri
139	9	3.2	271	2	Q8RHK9	Q8rhk9 fusobacteri	212	9	3.2	726	2	Q32971	Q32971 mycobacteri
140	9	3.2	272	2	Q7V306	Q7v306 prochloroco	213	9	3.2	749	2	Q8KJR6	Q8kjr6 gordonia ap
141	9	3.2	278	2	Q9Z9J3	Q9z9j3 bacillus ha	214	9	3.2	945	2	Q9N8D9	Q9n8d9 trypanosoma
142	9	3.2	279	2	Q6ASX4	Q6asx4 oryza sativ	215	9	3.2	948	2	Q85ZU4	Q85zu4 borrelia ga
143	9	3.2	279	2	Q748K0	Q748k0 geobacter s	216	9	3.2	950	2	Q51770	Q51770 borrelia bu
144	9	3.2	280	2	Q68106	Q68106 rhodobacter	217	9	3.2	960	2	Q73V82	Q73v82 mycobacteri
145	9	3.2	281	2	Q7Y189	Q7y189 oryza sativ	218	9	3.2	1031	2	Q7URK7	Q7urk7 rhodopirell
146	9	3.2	282	2	Q74L62	Q74l62 lactobacill	219	9	3.2	1175	2	Q8XNW6	Q8xnw6 clostridium
147	9	3.2	285	2	Q29256	Q29256 archaeoglob	220	9	3.2	1222	2	Q8KDA7	Q8kda7 chlorobium
148	9	3.2	286	2	Q99548	Q99548 staphylococ	221	9	3.2	1465	2	Q70WG4	Q70wg4 barley yell
149	9	3.2	286	2	Q7A088	Q7a088 staphylococ	222	9	3.2	2258	1	POL1_BAMMN	P90245 b genome po
150	9	3.2	286	2	Q7A471	Q7a471 staphylococ	223	9	3.2	2258	2	Q55459	Q55459 barley mild
151	9	3.2	286	2	Q6G7A0	Q6g7a0 staphylococ	224	9	3.2	2258	2	Q93128	Q93128 barley mild
152	9	3.2	286	2	Q6GEL4	Q6gel4 staphylococ	225	9	3.2	2258	2	Q65654	Q65654 barley mild
153	9	3.2	288	2	Q9KFX3	Q9kf34 bacillus ha	226	9	3.2	2258	2	Q68VH7	Q68vh7 barley mild
154	9	3.2	289	2	Q7NNH5	Q7nnh5 gloebacter	227	9	3.2	2258	2	Q68VH8	Q68vh8 barley mild
155	9	3.2	290	2	Q634W2	Q634w2 bacillus ce	228	9	3.2	2258	2	Q68VH9	Q68vh9 barley mild
156	9	3.2	290	2	Q730W8	Q730w8 bacillus ce	229	9	3.2	2258	2	Q9WAA3	Q9waa3 barley mild
157	9	3.2	290	2	Q818M8	Q818m8 bacillus ce	230	9	3.2	2261	2	Q71BF1	Q71bf1 barley mild
158	9	3.2	290	2	Q81M11	Q81m11 bacillus an	231	9	3.2	2404	2	Q9QBG1	Q9qbg1 wheat yello
159	9	3.2	290	2	Q6HDU2	Q6hd2 bacillus th	232	9	3.2	2404	2	Q9QBG4	Q9qbg4 wheat yello
160	9	3.2	292	2	Q8EG59	Q8eg59 shewanella	233	9	3.2	2407	2	Q9QMA1	Q9qma1 wheat yello
161	9	3.2	293	2	Q8YTP2	Q8ytp2 anabaena sp	234	9	3.2	2410	1	POL1_BAYMJ	Q01206 b genome po
162	9	3.2	294	2	Q9A2J5	Q9a2j5 caulobacter	235	9	3.2	2410	2	Q9YJW3	Q9yjlw3 barley yell
163	9	3.2	295	2	Q8GF30	Q8gf30 zymomonas m	236	9	3.2	2411	2	Q71BD5	Q71bd5 barley yell
164	9	3.2	296	2	Q897T0	Q897t0 clostridium	237	9	3.2	2412	1	POL1_BAYNG	Q04574 b genome po
165	9	3.2	297	2	Q8CPN7	Q8cpn7 xanthomonas	238	9	3.2	2412	2	Q70WS1	Q70ws1 barley yell
166	9	3.2	301	2	Q8CU34	Q8cu34 staphylococ	239	9	3.2	2412	2	Q70WS2	Q70ws2 barley yell
167	9	3.2	302	2	Q8NLB0	Q8nlb0 corynebacte	240	9	3.2	2412	2	Q70WS3	Q70ws3 barley yell
168	9	3.2	303	2	Q6NH47	Q6nh47 corynebacte	241	9	3.2	2412	2	Q70WS4	Q70ws4 barley yell
169	9	3.2	305	2	Q6M1H8	Q6m1h8 corynebacte	242	9	3.2	2412	2	Q70WS5	Q70ws5 barley yell
170	9	3.2	306	2	Q643B2	Q643b2 streptomyce	243	9	3.2	2412	2	Q70WS6	Q70ws6 barley yell
171	9	3.2	330	2	Q83H10	Q83h10 tropheryma	244	9	3.2	2412	2	Q70WS7	Q70ws7 barley yell
172	9	3.2	345	2	Q9AT00	Q9at00 arabidopsis	245	8	2.9	409	2	Q8XL26	Q8xl26 clostridium
173	9	3.2	346	2	Q83GR9	Q83gr9 tropheryma	246	8	2.9	108	2	Q9F6K2	Q9f6k2 brucella ab
174	9	3.2	364	2	Q80812	Q80812 arabidopsis	247	8	2.9	116	2	Q9QUT1	Q9qut1 mus musculus
175	9	3.2	472	2	Q7CUM3	Q7cum3 agrobacteri	248	8	2.9	208	1	URK_CLOPE	Q8xji6 clostridium
176	9	3.2	496	2	Q669F1	Q669f1 yersinia ps	249	8	2.9	212	2	Q892J8	Q892j8 clostridium
177	9	3.2	496	2	Q82DQ6	Q82dq6 yersinia pe	250	8	2.9	213	2	Q88UY6	Q88uy6 lactobacill

251	8	2.9	215	1	CCWA_BRUME	Q8vems brucella me	324	8	2.9	307	2	Q6NFA4	Q6nfa4 corynebacte
252	8	2.9	215	1	CCWA_BRUSU	Q8g358 brucella su	325	8	2.9	308	2	Q62GD4	Q62gd4 burkholderi
253	8	2.9	215	1	I12A_MOUSE	P43431 mus musculu	326	8	2.9	308	2	Q91008	Q91008 streptomyce
254	8	2.9	216	2	Q9K1R3	Q9k1r3 neisseria m	327	8	2.9	311	2	Q9A3C4	Q9a3c4 caulobacter
255	8	2.9	222	2	Q7VI23	Q7vi23 helicobacte	328	8	2.9	313	2	Q63Q81	Q63q81 burkholderi
256	8	2.9	224	2	Q7N0N3	Q7n0n3 photorhabdu	329	8	2.9	319	2	Q9HK71	Q9hk71 thermoplasma
257	8	2.9	226	2	Q8XN98	Q8xn98 clostridium	330	8	2.9	321	2	Q974E9	Q974e9 sulfobobus
258	8	2.9	229	2	Q10689	Q10689 cymbidium m	331	8	2.9	321	2	Q8XV75	Q8xv75 ralistonia s
259	8	2.9	229	2	Q6PY93	Q6py93 cymbidium m	332	8	2.9	334	2	Q6ARS3	Q6ars3 desulfotale
260	8	2.9	229	2	Q705K6	Q705k6 cymbidium m	333	8	2.9	334	2	Q8VQL8	Q8vql8 brucella ab
261	8	2.9	230	2	Q7VHG6	Q7vhg6 helicobacte	334	8	2.9	358	2	Q8PD85	Q8pd85 xanthomonas
262	8	2.9	231	2	Q7VHG6	Q7vhg6 helicobacte	335	8	2.9	377	2	Q8YDI3	Q8ydi3 brucella me
263	8	2.9	231	2	Q8UCS3	Q8ucs3 agrobacteri	336	8	2.9	382	2	Q99ZS8	Q99zs8 streptococc
264	8	2.9	233	2	Q37154	Q37154 cymbidium m	337	8	2.9	384	2	Q99ZS8	Q99zs8 streptococc
265	8	2.9	233	2	Q9Q3U7	Q9q3u7 cymbidium m	338	8	2.9	384	2	Q7CN92	Q7cn92 streptococc
266	8	2.9	234	2	Q74DH5	Q74dh5 geobacter s	339	8	2.9	384	2	Q8DUF7	Q8duf7 streptococc
267	8	2.9	237	2	Q30194	Q30194 archaeoglob	340	8	2.9	384	2	Q8DZJ0	Q8dzj0 streptococc
268	8	2.9	238	2	Q97MF3	Q97mf3 clostridium	341	8	2.9	384	2	Q8E554	Q8e554 streptococc
269	8	2.9	239	2	Q8CUI3	Q8cuy3 oceanobacil	342	8	2.9	385	2	Q8E554	Q8e554 streptococc
270	8	2.9	243	2	Q8NR42	Q8nr42 corynebacte	343	8	2.9	385	2	Q8DPC2	Q8dpc2 streptococc
271	8	2.9	243	2	Q8PT24	Q8pt24 bradyrhizob	344	8	2.9	390	2	Q8ZS21	Q8zs21 anabaena sp
272	8	2.9	244	2	Q7NNW9	Q7nnw9 geobacter	345	8	2.9	406	2	Q89B71	Q89b71 bradyrhizob
273	8	2.9	246	2	Q612U3	Q612u3 bacillus an	346	8	2.9	407	2	Q9YOH0	Q9yoh0 tetrahymena
274	8	2.9	248	2	Q29435	Q29435 archaeoglob	347	8	2.9	416	2	Q9YOH5	Q9yoh5 tetrahymena
275	8	2.9	248	2	Q8UAL3	Q8ual3 agrobacteri	348	8	2.9	420	2	Q9YFE1	Q9yfe1 aeropyrum p
276	8	2.9	249	2	Q9AX28	Q9ax28 oryza sativ	349	8	2.9	428	2	Q9CGD4	Q9cgd4 lactococcus
277	8	2.9	249	2	Q06529	Q06529 lactobacill	350	8	2.9	448	2	Q6FQ90	Q6fq90 candida gla
278	8	2.9	249	2	Q9FCU6	Q9fcu6 lactobacill	351	8	2.9	474	2	Q8PQ56	Q8pq56 xanthomonas
279	8	2.9	249	2	Q74DN5	Q74dn5 geobacter s	352	8	2.9	484	2	Q7VF91	Q7vf91 helicobacte
280	8	2.9	250	1	PS7B_PYRAE	Q8zx91 pyrobaculum	353	8	2.9	494	2	Q7CEQ8	Q7ceq8 streptococc
281	8	2.9	250	2	Q8VUH2	Q8vuh2 streptococc	354	8	2.9	506	2	Q9PPT0	Q9ppt0 methanosarc
282	8	2.9	250	2	Q731L0	Q731l0 treponema d	355	8	2.9	506	2	Q9PPT0	Q9ppt0 ureaplasma
283	8	2.9	250	2	Q8DUD2	Q8dud2 streptococc	356	8	2.9	507	2	Q6LUY1	Q6luy1 photobacter
284	8	2.9	250	2	Q8DX11	Q8dx11 streptococc	357	8	2.9	507	2	Q8UAZ4	Q8uaz4 agrobacteri
285	8	2.9	250	2	Q8ESM1	Q8esm1 streptococc	358	8	2.9	510	2	Q663Y5	Q663y5 yersinia ps
286	8	2.9	250	2	Q8UCH3	Q8uch3 agrobacteri	359	8	2.9	510	2	Q829Z3	Q829z3 yersinia pe
287	8	2.9	251	2	Q8TS12	Q8ts12 methanosarc	360	8	2.9	513	2	Q6DB03	Q6db03 clostridium
288	8	2.9	252	2	Q97085	Q97085 propionibac	361	8	2.9	514	2	Q894X5	Q894x5 salmonella
289	8	2.9	255	2	Q6ABL6	Q6abl6 propionibac	362	8	2.9	518	2	Q8L241	Q8l241 escherichia
290	8	2.9	255	2	Q7MBY2	Q7mby2 wolfinella s	363	8	2.9	523	2	Q8YOM7	Q8yom7 ralistonia s
291	8	2.9	256	2	Q62H61	Q62h61 burkholderi	364	8	2.9	527	2	Q7P2D6	Q7p2d6 fusobacteri
292	8	2.9	256	2	Q63R21	Q63r21 burkholderi	365	8	2.9	527	2	Q8RHU5	Q8rhu5 fusobacteri
293	8	2.9	257	2	Q8VVF9	Q8vvf9 streptococc	366	8	2.9	527	2	Q8RHP12	Q8rhp12 vibrio chol
294	8	2.9	257	2	Q8VVG3	Q8vvg3 streptococc	367	8	2.9	540	2	Q81HE3	Q81he3 bacillus ce
295	8	2.9	258	2	Q9K468	Q9k468 streptomyce	368	8	2.9	541	2	Q8NXX3	Q8nx3 staphylococ
296	8	2.9	258	2	Q6AIP0	Q6aip0 desulfotale	369	8	2.9	543	2	Q932E9	Q932e9 staphylococ
297	8	2.9	259	2	Q97E47	Q97e47 clostridium	370	8	2.9	543	2	Q99VT7	Q99vt7 staphylococ
298	8	2.9	259	2	Q9CET4	Q9cet4 lactococcus	371	8	2.9	543	2	Q6GBE6	Q6gbe6 staphylococ
299	8	2.9	260	2	Q6A7M6	Q6a7m6 propionibac	372	8	2.9	543	2	Q6GIV8	Q6giv8 staphylococ
300	8	2.9	262	2	Q73NH4	Q73nh4 treponema d	373	8	2.9	549	2	Q62J78	Q62j78 burkholderi
301	8	2.9	263	2	Q880B4	Q880b4 pseudomonas	374	8	2.9	549	2	Q63SX1	Q63sx1 burkholderi
302	8	2.9	263	2	Q9RKT3	Q9rkt3 streptomyce	375	8	2.9	549	2	Q98K72	Q98k72 rhizobium l
303	8	2.9	265	2	Q9S1F1	Q9s1f1 vibrio chol	376	8	2.9	549	2	Q7WNN2	Q7wnn2 bordetella
304	8	2.9	269	2	Q89H05	Q89h05 bradyrhizob	377	8	2.9	550	2	Q6ANY7	Q6any7 desulfotale
305	8	2.9	274	2	Q8V5U5	Q8v5u5 listeria mo	378	8	2.9	551	2	Q6A6S5	Q6a6s5 propionibac
306	8	2.9	274	2	Q92A48	Q92a48 listeria mo	379	8	2.9	552	2	Q6LPY6	Q6lpv6 photobacter
307	8	2.9	274	2	Q71Y54	Q71y54 listeria mo	380	8	2.9	554	2	Q7QN86	Q7qn86 anopheles g
308	8	2.9	275	2	Q7CS95	Q7cs95 agrobacteri	381	8	2.9	554	2	Q6ACM0	Q6acm0 leifsonia x
309	8	2.9	278	2	Q6LX68	Q6lx68 methanococc	382	8	2.9	555	2	Q89P20	Q89p20 bradyrhizob
310	8	2.9	278	2	Q882J7	Q882j7 pseudomonas	383	8	2.9	556	2	Q9K5W6	Q9k5w6 bacillus ha
311	8	2.9	280	2	Q82LM9	Q82lm9 streptomyce	384	8	2.9	557	2	Q9K5W6	Q9k5w6 bacillus ha
312	8	2.9	281	2	Q8XHV2	Q8xhv2 clostridium	385	8	2.9	560	2	Q74IR3	Q74ir3 lactobacill
313	8	2.9	283	2	Q7W2Y9	Q7w2y9 bordetella	386	8	2.9	564	2	Q8CTJ5	Q8ctj5 staphylococ
314	8	2.9	283	2	Q7WDY9	Q7wdy9 bordetella	387	8	2.9	568	2	Q73HY8	Q73hy8 wolbachia p
315	8	2.9	283	2	Q83DG0	Q83dg0 coxiella bu	388	8	2.9	569	2	Q88H94	Q88h94 pseudomonas
316	8	2.9	287	2	Q67JX3	Q67jx3 symbiobacte	389	8	2.9	571	2	Q54121	Q54121 staphylococ
317	8	2.9	289	2	Q9F1W2	Q9f1w2 streptomyce	390	8	2.9	578	2	Q73X96	Q73x96 pyrococcus
318	8	2.9	289	2	Q6FFK1	Q6ffk1 acinetobact	391	8	2.9	581	2	Q8UOD8	Q8uod8 pyrococcus
319	8	2.9	291	2	Q8PA14	Q8pa14 xanthomonas	392	8	2.9	581	2	Q74HD4	Q74hd4 lactobacill
320	8	2.9	291	2	Q8PM85	Q8pm85 xanthomonas	393	8	2.9	581	2	Q8PF61	Q8pf61 corynebacte
321	8	2.9	298	2	Q9REN4	Q9ren4 zymomonas m	394	8	2.9	583	1	EXP8_STRPN	P35598 streptococc
322	8	2.9	298	2	Q892V1	Q892v1 clostridium	395	8	2.9	583	2	Q9URY4	Q9ury4 schizosacch
323	8	2.9	300	2	Q7P0X8	Q7p0x8 chromobacte	396	8	2.9	583	2	Q8DNL4	Q8dnl4 streptococc

397	8	2.9	588	2	Q7NCV8	Q7ncv8 gloeobacter	470	7	2.5	88	1	RS15_PHOLU	P41120 photorhabdu
398	8	2.9	589	2	Q8RGT4	Q8rgt4 fusobacteri	471	7	2.5	89	2	Q9N9Q1	Q9n9q1 leishmania
399	8	2.9	589	2	Q8EV13	Q8ev13 mycoplasma	472	7	2.5	89	2	Q9AMN7	Q9awn7 oryza sativ
400	8	2.9	590	2	Q8P8R0	Q8per0 methanosarc	473	7	2.5	89	2	Q7MYT9	Q7myy9 photorhabdu
401	8	2.9	590	2	Q7V0Z5	Q7v0z5 prochloroco	474	7	2.5	94	2	Q8DT21	Q8dtt21 streptococc
402	8	2.9	594	2	Q834D4	Q834d4 enterococcu	475	7	2.5	95	1	Y736_ARCFU	Q29522 archaesoglob
403	8	2.9	595	2	Q30410	Q30410 bacillus br	476	7	2.5	109	2	Q9B034	Q9b034 bacteriophag
404	8	2.9	595	2	Q82WGO	Q82wgo nitrosomona	477	7	2.5	111	2	Q9DB78	Q9db78 mus musculu
405	8	2.9	596	1	ABCL_ENCCU	Q8eq15 encephalito	478	7	2.5	119	2	Q30353	Q30353 cervus elap
406	8	2.9	600	2	Q8SQV1	Q8sqv1 encephalito	479	7	2.5	123	2	Q67MY3	Q67my3 symbiobacte
407	8	2.9	600	2	Q93GX8	Q93gx8 streptomyc	480	7	2.5	126	2	Q6LNU3	Q6lnz3 photobacter
408	8	2.9	600	2	Q7NBB3	Q7nbb3 mycoplasma	481	7	2.5	127	2	Q96MJ2	Q96mj2 homo sapien
409	8	2.9	601	2	Q8Y6N3	Q8y6n3 listeria mo	482	7	2.5	132	2	Q65X68	Q65x68 oryza sativ
410	8	2.9	601	2	Q82B59	Q82b59 listeria in	483	7	2.5	134	2	Q982A2	Q982a2 streptomyc
411	8	2.9	601	2	Q71Z19	Q71z19 listeria mo	484	7	2.5	137	2	Q67RT2	Q67rt2 symbiobacte
412	8	2.9	603	2	Q7MJF9	Q7mjf9 vibrio vuln	485	7	2.5	142	2	Q8W60	Q8w60 homo sapien
413	8	2.9	604	2	Q6AAP8	Q6aaf8 propionibac	486	7	2.5	143	1	COTP_BACSU	P96698 bacillus su
414	8	2.9	606	2	Q44940	Q44940 drosophila	487	7	2.5	147	2	Q9KK03	Q9kk03 pseudomonas
415	8	2.9	606	2	Q8SX41	Q8sx41 drosophila	488	7	2.5	148	2	Q7N0M8	Q7n0m8 photorhabdu
416	8	2.9	606	2	Q7KWB2	Q7kwb2 drosophila	489	7	2.5	150	2	Q8DP35	Q8dp35 streptococc
417	8	2.9	606	2	Q8YMH8	Q8ymh8 anabaena sp	490	7	2.5	151	2	Q9ANS4	Q9ans4 rhodobacter
418	8	2.9	607	2	Q6Y8R0	Q6y8r0 mycoplasma	491	7	2.5	153	2	Q6M0J2	Q6m0j2 methanococc
419	8	2.9	608	2	Q73JW5	Q73jw5 treponema d	492	7	2.5	154	2	Q6G1F3	Q6g1f3 bartonella
420	8	2.9	608	2	Q9CG38	Q9cg38 lactococcus	493	7	2.5	155	2	Q7QRK5	Q7qrk5 giardia lam
421	8	2.9	614	2	Q8TQ05	Q8tq05 methanosarc	494	7	2.5	157	2	Q860L5	Q860l5 syncerus ca
422	8	2.9	614	2	Q8F141	Q8f141 mesoplasma	495	7	2.5	158	2	Q8L490	Q8l490 oryza sativ
423	8	2.9	626	2	Q7NIB9	Q7nib9 gloeobacter	496	7	2.5	158	2	Q67JD2	Q67jd2 symbiobacte
424	8	2.9	636	2	Q9S368	Q9s368 neisseria g	497	7	2.5	162	2	Q19804	Q19804 caenorhabdi
425	8	2.9	636	2	Q9XAZ9	Q9xaz9 neisseria g	498	7	2.5	162	2	Q82RA8	Q82ra8 streptomyc
426	8	2.9	636	2	Q9JZH4	Q9jzh4 neisseria m	499	7	2.5	167	2	Q9AKT6	Q9akt6 paenibacill
427	8	2.9	646	2	Q84266	Q84266 chlamydia t	500	7	2.5	168	2	Q6CUI3	Q6cui3 kluyveromyc
428	8	2.9	646	2	Q8WC12	Q8wc12 parachlamyd	501	7	2.5	170	2	Q6PYC4	Q6pyc4 rhizobium m
429	8	2.9	647	2	Q9PKD0	Q9pkd0 chlamydia m	502	7	2.5	171	2	Q7ZST0	Q7zst0 human immun
430	8	2.9	650	2	Q8Y5I9	Q8y5i9 listeria mo	503	7	2.5	172	2	Q6D354	Q6d354 erwinia car
431	8	2.9	650	2	Q929U5	Q929u5 listeria in	504	7	2.5	174	2	Q8YL81	Q8yl81 anabaena sp
432	8	2.9	650	2	Q71XU0	Q71xu0 listeria mo	505	7	2.5	174	2	Q97RH8	Q97rh8 streptococc
433	8	2.9	666	2	Q63FP6	Q63fp6 bacillus ce	506	7	2.5	175	2	Q8BPZ5	Q8bpz5 mus musculu
434	8	2.9	666	2	Q73CX1	Q73cx1 bacillus ce	507	7	2.5	176	1	ABOK_MYCTU	P95014 mycobacteri
435	8	2.9	666	2	Q6HMH8	Q6hmh8 bacillus th	508	7	2.5	176	2	Q74LJ8	Q74lj8 mycobacteri
436	8	2.9	672	2	Q65LV8	Q65lv8 bacillus li	509	7	2.5	176	2	Q7MGV9	Q7mgv9 vibrio vuln
437	8	2.9	673	2	Q07549	Q07549 bacillus su	510	7	2.5	176	2	Q8DCY7	Q8dcy7 vibrio vuln
438	8	2.9	674	2	Q9KDD3	Q9kdd3 bacillus ha	511	7	2.5	178	2	Q6AGS6	Q6ag56 leifsonia x
439	8	2.9	676	2	Q8CUK8	Q8cuk8 oceanobacil	512	7	2.5	180	2	Q6CZF6	Q6czf6 erwinia car
440	8	2.9	677	2	Q9H0G8	Q9h0g8 arabidopsis	513	7	2.5	181	2	P71891	P71891 mycobacteri
441	8	2.9	678	2	Q9FUT3	Q9fut3 arabidopsis	514	7	2.5	181	2	Q7TYT9	Q7tyt9 mycobacteri
442	8	2.9	680	2	Q9M0G9	Q9m0g9 arabidopsis	515	7	2.5	183	2	Q8UBK1	Q8ubk1 agrobacteri
443	8	2.9	690	1	ATM1_YEAST	P40416 saccharomyc	516	7	2.5	185	2	Q8PD12	Q8pd12 xanthomonas
444	8	2.9	691	2	Q751N2	Q751n2 ashbya gos	517	7	2.5	187	2	Q6FUA4	Q6fua4 candida gla
445	8	2.9	696	2	Q6BXD7	Q6bxd7 debaryomyc	518	7	2.5	188	1	Y176_SULTO	Q97615 sulfolobus
446	8	2.9	710	2	Q6C6N0	Q6c6n0 yarrowia li	519	7	2.5	189	1	RUVA_WOLSU	Q7ma70 wolfinella s
447	8	2.9	720	2	Q6CX96	Q6cx96 kluyveromyc	520	7	2.5	189	2	Q704N6	Q704n6 sugarcane y
448	8	2.9	722	2	Q9F445	Q9f445 streptococc	521	7	2.5	190	2	Q970B3	Q970b3 sulfolobus
449	8	2.9	727	2	Q6FMS9	Q6fms9 candida gla	522	7	2.5	191	2	Q8KCL0	Q8kcl0 chlorobium
450	8	2.9	728	2	Q9LPF8	Q9lpf8 arabidopsis	523	7	2.5	197	1	CYC1_BACSU	Q34577 bacillus su
451	8	2.9	728	2	Q9LVM1	Q9lvm1 arabidopsis	524	7	2.5	197	2	Q65JT8	Q65jt8 bacillus li
452	8	2.9	733	2	Q658I3	Q658i3 oryza sativ	525	7	2.5	200	2	Q7P7R5	Q7p7r5 fusobacteri
453	8	2.9	738	2	Q6D228	Q6d228 erwinia car	526	7	2.5	200	2	Q8UJF5	Q8ujf5 agrobacteri
454	8	2.9	756	2	Q8BX70	Q8bx70 lactobacill	527	7	2.5	201	1	COAB_CLOB	Q97k22 clostridium
455	8	2.9	767	2	Q8NZE2	Q8nze2 streptococc	528	7	2.5	201	2	Q8AAQ1	Q8aaq1 bacteroides
456	8	2.9	781	2	Q7QWE0	Q7qwe0 giardia lam	529	7	2.5	202	2	Q64VR1	Q64vr1 bacteroides
457	8	2.9	788	2	Q73FZ8	Q73fz8 wolbachia p	530	7	2.5	204	1	KGUA_BACTN	Q8a677 bacteroides
458	8	2.9	810	2	Q8G838	Q8g838 bifidobacte	531	7	2.5	204	2	Q64PY1	Q64py1 bacteroides
459	8	2.9	820	2	Q9KEY5	Q9key5 bacillus ha	532	7	2.5	205	2	Q99ZT5	Q99zt5 streptococc
460	8	2.9	1062	2	Q6VTH1	Q6vth1 chlamydomon	533	7	2.5	206	1	COAB_PASMU	Q9cpf5 pasteurella
461	8	2.9	1167	1	CARB_RHILO	Q98187 rhizobium l	534	7	2.5	206	1	CYSC_BUCAI	P57497 buchnera ap
462	8	2.9	1177	2	Q8RCY8	Q8rcy8 thermoaer	535	7	2.5	206	2	Q8YQ85	Q8yq85 anabaena sp
463	8	2.9	1293	2	Q9V748	Q9v748 emericella	536	7	2.5	206	2	Q9QSB4	Q9qsb4 human immun
464	8	2.9	1318	2	Q9VJ21	Q9vj21 drosophila	537	7	2.5	207	1	CYSC_LACPL	Q88x60 lactobacill
465	8	2.9	1323	1	HST6_CANAL	P53706 candida alb	538	7	2.5	207	2	Q9PAT3	Q9fat3 vibrio para
466	8	2.9	1637	2	Q9VRG5	Q9vr95 drosophila	539	7	2.5	208	1	COAB_WIGER	Q8d308 wiggleswort
467	7	2.5	52	2	Q6KEB8	Q6keb8 homo sapien	540	7	2.5	208	1	CYC2_BACHD	Q9k7h6 bacillus ha
468	7	2.5	52	2	Q71V93	Q71v93 ovis aries	541	7	2.5	209	1	LOLB_HAEIN	P45270 haemophilus
469	7	2.5	68	2	Q69619	Q69619 human immun	542	7	2.5	209	1	URK_CLOTE	Q896e3 clostridium

543	7	2.5	212	2	Q7U576	Q7U576	synechococ	616	7	2.5	238	1	ZNUC_BUCBP	Q89aj0	buchnera ap
544	7	2.5	212	2	Q9UJQ4	Q9Jjq4	mus musculu	617	7	2.5	239	2	Q860K6	Q860k6	traglephus
545	7	2.5	214	2	Q65VP4	Q65vp4	mannheimia	618	7	2.5	240	1	Y124_THEMA	Q9wx8	thermotoga
546	7	2.5	215	2	Q9JJQ7	Q9jjq7	mus musculu	619	7	2.5	240	2	Q18131	Q18131	caenorhabdi
547	7	2.5	215	2	Q9JJQ8	Q9jjq8	mus musculu	620	7	2.5	240	2	Q2NDL2	Q2ndl2	listeria in
548	7	2.5	216	2	Q65Y02	Q65y02	bombyx mori	621	7	2.5	240	2	Q6N749	Q6n749	rhodospseudo
549	7	2.5	216	2	Q8EWH7	Q8ewh7	mycoplasma	622	7	2.5	240	2	Q6D1A9	Q6dia9	erwinia car
550	7	2.5	217	2	Q8SSJ6	Q8ssj6	encephalico	623	7	2.5	244	2	Q6UP75	Q6up75	alcaligenes
551	7	2.5	218	1	KC1_FUSNN	Q8rii8	fusobacteri	624	7	2.5	244	2	Q87JR9	Q87jr9	fusobacteri
552	7	2.5	218	2	Q8TZW8	Q8tzw8	pyrococcus	625	7	2.5	244	2	Q87JTS	Q87jts	vibrio para
553	7	2.5	219	2	Q8ZXP8	Q8zxp8	pyrobaculum	626	7	2.5	245	2	Q7DM58	Q7dm58	arabidopsis
554	7	2.5	219	2	Q750E1	Q750e1	ashbya goss	627	7	2.5	245	2	Q6M391	Q6m391	corynebacte
555	7	2.5	219	2	Q7P7N3	Q7p7n3	fusobacteri	628	7	2.5	245	2	Q81X89	Q81x89	bacillus an
556	7	2.5	220	2	Q926L8	Q926l8	listeria in	629	7	2.5	246	1	NATA_BACSU	P46903	bacillus eu
557	7	2.5	222	2	Q87TW3	Q87tw3	pseudomonas	630	7	2.5	246	2	Q6MLX6	Q6mlx6	bdellovibri
558	7	2.5	222	2	Q8FTL1	Q8ftl1	corynebacte	631	7	2.5	247	2	Q8ZVX1	Q8zvx1	pyrobaculum
559	7	2.5	223	1	GIDB_CORGL	Q8nl53	corynebacte	632	7	2.5	247	2	Q81EP0	Q81ep0	mesoplasma
560	7	2.5	223	2	Q7X057	Q7x057	uncultured	633	7	2.5	247	2	Q6FILL1	Q6fll1	streptomyce
561	7	2.5	223	2	Q6YQY4	Q6yqy4	onion yello	634	7	2.5	248	2	Q829V5	Q829v5	methyllobact
562	7	2.5	224	1	YJ07_SYNEL	Q8dym8	synechococ	635	7	2.5	249	2	Q8GEK2	Q8gek2	corynebacte
563	7	2.5	224	2	Q8RDY9	Q8rdy9	fusobacteri	636	7	2.5	249	2	Q8NN48	Q8nn48	agrobacteri
564	7	2.5	225	2	Q65TW5	Q65tw5	mannheimia	637	7	2.5	249	2	Q8UJE3	Q8uje3	rhodospseudo
565	7	2.5	225	2	Q8W82	Q8w82	lactobacill	638	7	2.5	249	2	Q6N2L3	Q6n2l3	geobacter s
566	7	2.5	226	2	Q8GP10	Q8gp10	staphylococ	639	7	2.5	250	2	Q748L6	Q748l6	wohinella s
567	7	2.5	227	1	CORE_CLOTE	Q89j5	clostridium	640	7	2.5	250	2	Q7MAP5	Q7map5	escherichia
568	7	2.5	227	2	Q6BUE9	Q6bue9	debaromyce	641	7	2.5	251	1	ZNUC_ECOLI	P52648	salmonella
569	7	2.5	228	2	Q7V2N9	Q7v2n9	prochloroco	642	7	2.5	251	2	Q8Z5W6	Q8z5w6	bradyrhizob
570	7	2.5	228	2	Q8ETU3	Q8etu3	oceanobacil	643	7	2.5	251	2	Q89GM2	Q89gm2	bradyrhizob
571	7	2.5	229	2	Q883F0	Q883f0	pseudomonas	644	7	2.5	251	2	Q8SQE2	Q8sqe2	bifidobacte
572	7	2.5	230	2	Q97414	Q97414	sulfolobus	645	7	2.5	251	2	Q8G582	Q8g582	deinococcus
573	7	2.5	230	2	Q7P6R9	Q7p6r9	fusobacteri	646	7	2.5	251	2	Q9RY19	Q9ry19	photobacter
574	7	2.5	230	2	Q6SK67	Q6sk67	bacillus li	647	7	2.5	252	2	Q83KR7	Q83kr7	shigella fl
575	7	2.5	230	2	Q31711	Q31711	bacillus su	648	7	2.5	252	2	Q6LI01	Q6li01	bdellovibri
576	7	2.5	230	2	Q8NVX0	Q8nvx0	staphylococ	649	7	2.5	252	2	Q6MGW2	Q6mgw2	bdellovibri
577	7	2.5	230	2	Q6G8B6	Q6g8b6	staphylococ	650	7	2.5	252	2	Q6MPE0	Q6mpe0	erwinia car
578	7	2.5	231	2	Q6GVN5	Q6gvn5	rhizobium l	651	7	2.5	253	1	PSTB_PYRAB	Q6d48	pyrococcus
579	7	2.5	231	2	Q98W31	Q98w31	mycobacteri	652	7	2.5	253	1	PSTB_PYRFU	Q8u247	pyrococcus
580	7	2.5	231	2	Q73S69	Q73s69	bradyrhizob	653	7	2.5	253	2	Q66AT7	Q66at7	versinia ps
581	7	2.5	231	2	Q89EU1	Q89eu1	agrobacteri	654	7	2.5	253	2	Q82EU3	Q82eu3	versinia pe
582	7	2.5	232	2	Q8UJE2	Q8uje2	agrobacteri	655	7	2.5	253	2	Q99WR6	Q99wr6	staphylococ
583	7	2.5	232	2	Q8YVM7	Q8yvm7	anabaena sp	656	7	2.5	253	2	Q740F8	Q740f8	methanosarc
584	7	2.5	232	2	Q74LK0	Q74lk0	lactobacill	657	7	2.5	253	2	Q83189	Q83189	methanosarc
585	7	2.5	233	2	Q7P429	Q7p429	fusobacteri	658	7	2.5	254	2	Q8TR44	Q8tr44	aeropyrum p
586	7	2.5	233	2	Q7DBB3	Q7ddb3	neisseria m	659	7	2.5	254	2	Q9YDJ4	Q9yjd4	porphyromon
587	7	2.5	233	2	Q9JRA3	Q9jra3	neisseria m	660	7	2.5	254	2	Q7MM92	Q7mm92	oceanobacil
588	7	2.5	234	2	Q70824	Q70824	hepatitis c	661	7	2.5	254	2	Q8ESF4	Q8esf4	hepatitis c
589	7	2.5	234	2	Q70825	Q70825	hepatitis c	662	7	2.5	254	2	Q8ESF4	Q8esf4	hepatitis c
590	7	2.5	234	2	Q70826	Q70826	hepatitis c	663	7	2.5	254	2	Q81585	Q81585	sulfolobus
591	7	2.5	234	2	Q70827	Q70827	hepatitis c	664	7	2.5	255	2	Q97WA2	Q97wa2	mycobacteri
592	7	2.5	234	2	Q70828	Q70828	hepatitis c	665	7	2.5	255	2	Q33189	Q33189	mycobacteri
593	7	2.5	234	2	Q70829	Q70829	hepatitis c	666	7	2.5	255	2	Q99TU0	Q99tu0	staphylococ
594	7	2.5	234	2	Q70830	Q70830	hepatitis c	667	7	2.5	255	2	Q7A0S6	Q7a0s6	staphylococ
595	7	2.5	234	2	Q70831	Q70831	hepatitis c	668	7	2.5	255	2	Q7A5D3	Q7a5d3	staphylococ
596	7	2.5	234	2	Q70832	Q70832	hepatitis c	669	7	2.5	255	2	Q7TZS5	Q7tzs5	mycobacteri
597	7	2.5	234	2	Q70833	Q70833	hepatitis c	670	7	2.5	256	2	Q8TKF8	Q8tkf8	methanosarc
598	7	2.5	234	2	Q70834	Q70834	hepatitis c	671	7	2.5	256	2	Q8KAQ1	Q8kaq1	chlorobium
599	7	2.5	234	2	Q70835	Q70835	hepatitis c	672	7	2.5	256	2	Q6N4P3	Q6n4p3	rhodospseudo
600	7	2.5	234	2	Q70836	Q70836	hepatitis c	673	7	2.5	256	2	Q73Q19	Q73q19	treponema d
601	7	2.5	234	2	Q70837	Q70837	hepatitis c	674	7	2.5	257	1	LIVG_METJA	Q5863	methanococc
602	7	2.5	234	2	Q70838	Q70838	hepatitis c	675	7	2.5	257	1	ORC6_DROME	Q9ylb2	drosophila
603	7	2.5	234	2	Q70839	Q70839	hepatitis c	676	7	2.5	257	2	P71508	P71508	methyllobact
604	7	2.5	234	2	Q70840	Q70840	hepatitis c	677	7	2.5	257	2	Q63CM2	Q63cm2	bacillus ce
605	7	2.5	234	2	Q70841	Q70841	hepatitis c	678	7	2.5	257	2	Q8XWN5	Q8xwn5	ralstonia s
606	7	2.5	234	2	Q70842	Q70842	hepatitis c	679	7	2.5	257	2	Q81RV4	Q81rv4	bacillus an
607	7	2.5	234	2	Q89254	Q89254	hepatitis c	680	7	2.5	257	2	Q6HK27	Q6hk27	halobacteri
608	7	2.5	234	2	Q89255	Q89255	hepatitis c	681	7	2.5	258	2	Q9HS04	Q9hs04	varrowia li
609	7	2.5	234	2	Q89256	Q89256	hepatitis c	682	7	2.5	258	2	Q6CFI6	Q6cfi6	fusobacteri
610	7	2.5	234	2	Q89256	Q89256	hepatitis c	683	7	2.5	259	2	Q6REJ2	Q6rei2	acinetobact
611	7	2.5	235	2	Q8TWT8	Q8twt8	methanopyru	684	7	2.5	259	2	Q6FFL0	Q6ffl0	pyrococcus
612	7	2.5	235	2	Q98LR7	Q98lr7	rhizobium l	685	7	2.5	259	2	Q6ADG4	Q6adg4	leifsonia x
613	7	2.5	236	2	Q9YDJ2	Q9yjd2	aeropyrum p	686	7	2.5	259	2	O57872	O57872	pyrococcus
614	7	2.5	238	1	ZNUC_BUCAI	P57403	buchnera ap	687	7	2.5	260	2			
615	7	2.5	238	1	ZNUC_BUCAP	Q8k9m6	buchnera ap	688	7	2.5	260	2			

689	7	2.5	260	2	Q8U4L3	Q8u4l3 pyrococcus
690	7	2.5	260	2	Q01842	Q01842 caenorhabdi
691	7	2.5	260	2	Q62IC1	Q62ic1 burkholderi
692	7	2.5	260	2	Q63WF1	Q63wf1 burkholderi
693	7	2.5	260	2	Q8RIR8	Q8rir8 fusobacteri
694	7	2.5	260	2	Q8RKC6	Q8rkcs streptomyce
695	7	2.5	261	2	Q26555	Q26555 methanobact
696	7	2.5	261	2	Q9R6G1	Q9r6g1 agrobacteri
697	7	2.5	261	2	Q9RGL9	Q9rgl9 staphylococ
698	7	2.5	261	2	Q9RQC6	Q9rqc6 zymomonas m
699	7	2.5	261	2	Q98GB7	Q98gb7 rhizobium l
700	7	2.5	261	2	Q6G910	Q6g910 staphylococ
701	7	2.5	261	2	Q6GGE3	Q6g9e3 staphylococ
702	7	2.5	261	2	Q8UB01	Q8ub01 agrobacteri
703	7	2.5	262	2	Q67RE7	Q67re7 symbiobacte
704	7	2.5	262	2	Q82HA2	Q82ha2 streptomyce
705	7	2.5	262	2	Q8DYG6	Q8dyg6 streptococc
706	7	2.5	262	2	Q8E429	Q8e429 streptococc
707	7	2.5	263	2	Q8TM86	Q8tm86 methanosarc
708	7	2.5	263	2	Q8TR20	Q8tr20 methanosarc
709	7	2.5	263	2	Q8CSE1	Q8cse1 staphylococ
710	7	2.5	263	2	Q10CP24	Q10cp24 pasteurella
711	7	2.5	264	2	Q8UC28	Q8uc28 agrobacteri
712	7	2.5	265	2	Q7N545	Q7n545 photorhabdu
713	7	2.5	266	2	Q7QNA3	Q7qn49 anopheles g
714	7	2.5	266	2	Q8XIK5	Q8xyk5 raistonia s
715	7	2.5	266	2	Q9WY65	Q9wy65 thermotoga
716	7	2.5	266	2	Q8UBX4	Q8ubx4 agrobacteri
717	7	2.5	268	1	ZNUC_HAEIN	P44692 haemophilus
718	7	2.5	268	2	Q8ZNV7	Q8znv7 salmonella
719	7	2.5	269	2	Q8XYT0	Q6xyt0 spiroplasma
720	7	2.5	269	2	Q8NVB5	Q8nvb5 staphylococ
721	7	2.5	269	2	Q9S847	Q9se47 staphylococ
722	7	2.5	269	2	Q7A470	Q7a470 staphylococ
723	7	2.5	269	2	Q8CRI6	Q8cri6 staphylococ
724	7	2.5	269	2	Q6G799	Q6g799 staphylococ
725	7	2.5	269	2	Q6GEL3	Q6gel3 staphylococ
726	7	2.5	270	2	Q630M0	Q630m0 bacillus ce
727	7	2.5	270	2	Q72X68	Q72x68 bacillus ce
728	7	2.5	270	2	Q814P3	Q814p3 bacillus ce
729	7	2.5	270	2	Q81J80	Q81j80 bacillus an
730	7	2.5	270	2	Q6HAQ5	Q6haq5 bacillus th
731	7	2.5	271	2	Q9X470	Q9x470 streptomyce
732	7	2.5	271	2	Q8JRV1	Q8jrv1 phthorimaea
733	7	2.5	272	2	Q9EX40	Q9ex40 streptomyce
734	7	2.5	273	2	Q91J3S2	Q91j3s2 anabaena sp
735	7	2.5	273	2	Q8RCQ9	Q8rcq9 thermoanaer
736	7	2.5	274	1	Y179_MYCGE	P47425 mycoplasma
737	7	2.5	274	1	Y179_MYCPN	Q50294 mycoplasma
738	7	2.5	274	2	Q7QMR0	Q7qmr0 anopheles g
739	7	2.5	274	2	Q7T517	Q7t517 cryptophleb
740	7	2.5	275	2	Q82E94	Q82e94 streptomyce
741	7	2.5	275	2	Q83FW1	Q83fw1 tropheryma
742	7	2.5	275	2	Q8S9J1	Q8sgj1 bradyrhizob
743	7	2.5	276	2	Q988C7	Q988c7 rhizobium l
744	7	2.5	276	2	Q9X8G3	Q9x8g3 streptomyce
745	7	2.5	277	2	Q7D2U3	Q7d2u3 agrobacteri
746	7	2.5	277	2	Q84204	Q84204 chlamydia t
747	7	2.5	278	1	ECUTJ_ECOLI	P77277 escherichia
748	7	2.5	278	2	Q66S28	Q66s28 oikopleura
749	7	2.5	278	2	Q8EF96	Q8ef96 escherichia
750	7	2.5	278	2	Q8XBH0	Q8xbh0 escherichia
751	7	2.5	278	2	Q86826	Q86826 hepatitis c
752	7	2.5	279	1	ECUTJ_SALTY	P41794 salmonella
753	7	2.5	279	2	Q8Y454	Q8y454 listeria mo
754	7	2.5	279	2	Q927N8	Q927n8 listeria in
755	7	2.5	279	2	Q97JB8	Q97jb8 clostridium
756	7	2.5	279	2	Q71WH7	Q71wh7 listeria mo
757	7	2.5	279	2	Q74JK2	Q74jk2 lactobacill
758	7	2.5	279	2	Q8ETV7	Q8etv7 oceanobact
759	7	2.5	280	1	CBIO_METTH	Q26236 methanobact
760	7	2.5	280	2	Q9V1Q4	Q9v1q4 pyrococcus
761	7	2.5	281	2	Q67MB5	Q67mb5 symbiobacte

762	7	2.5	281	2	Q9ZIC9	Q9zic9 listeria mo
763	7	2.5	281	2	Q9PKJ1	Q9pkj1 chlamydia m
764	7	2.5	281	2	Q6AFU1	Q6afu1 leifsonia x
765	7	2.5	282	2	Q8VIM1	Q8vim1 mus musculus
766	7	2.5	282	2	Q7TPU2	Q7tpu2 mus musculus
767	7	2.5	283	2	Q87CB3	Q87cb3 xylella fas
768	7	2.5	283	2	Q89F04	Q89f04 bradyrhizob
769	7	2.5	283	2	Q9PD02	Q9pd02 xylella fas
770	7	2.5	284	1	Y46B_MYCPN	Q50316 mycoplasma
771	7	2.5	284	2	Q59479	Q59479 pyrococcus
772	7	2.5	284	2	Q87316	Q87316 mycobacteri
773	7	2.5	284	2	Q9K245	Q9k245 chlamydia p
774	7	2.5	284	2	Q9Z8Y3	Q9z8y3 chlamydia p
775	7	2.5	284	2	Q81589	Q81589 hepatitis c
776	7	2.5	285	1	PANC_CAUCR	Q9a6c8 caulobacter
777	7	2.5	287	2	Q8PV82	Q8pv82 methanosarc
778	7	2.5	287	2	Q6MMA8	Q6mma8 bdellovibri
779	7	2.5	287	2	Q8EUF1	Q8euf1 mycoplasma
780	7	2.5	288	2	Q6XY24	Q6xy24 spiroplasma
781	7	2.5	288	2	Q822S5	Q822s5 chlamydophi
782	7	2.5	288	2	Q82G37	Q82g37 streptomyce
783	7	2.5	289	1	STAR_XENLA	Q6dg08 xenopus lae
784	7	2.5	289	2	Q6NHR4	Q6nhr4 corynebacte
785	7	2.5	289	2	Q89G67	Q89g67 bradyrhizob
786	7	2.5	289	2	Q9KZV3	Q9kzv3 streptomyce
787	7	2.5	290	2	Q7V156	Q7v156 helicobacte
788	7	2.5	291	2	Q87VM0	Q87vm0 pseudomonas
789	7	2.5	291	2	Q88DG1	Q88dg1 pseudomonas
790	7	2.5	292	2	Q84BI7	Q84bi7 streptococc
791	7	2.5	292	2	Q34641	Q34641 bacillus su
792	7	2.5	292	2	Q6MKT3	Q6mkt3 bdellovibri
793	7	2.5	292	2	Q72HG0	Q72hg0 thermus the
794	7	2.5	293	2	Q8NR37	Q8nr37 corynebacte
795	7	2.5	293	2	Q8R7Y4	Q8r7y4 thermoanaer
796	7	2.5	293	2	Q8DT43	Q8dt43 streptococc
797	7	2.5	294	2	Q9XCW9	Q9xcw9 rhodobacter
798	7	2.5	294	2	Q9PPV1	Q9ppv1 ureaplasma
799	7	2.5	296	2	Q67LV2	Q67lv2 symbiobacte
800	7	2.5	297	2	Q9CNM8	Q9cnm8 pasteurella
801	7	2.5	298	2	Q886U8	Q886u8 pseudomonas
802	7	2.5	299	2	Q68479	Q68479 achromobact
803	7	2.5	299	2	Q9R9K7	Q9r9k7 paracoccus
804	7	2.5	299	2	Q7SL01	Q7sl01 human immun
805	7	2.5	301	2	Q8TDQ0	Q8tdq0 homo sapien
806	7	2.5	301	2	Q96K94	Q96k94 homo sapien
807	7	2.5	302	2	Q69WA8	Q69wa8 oryza sativ
808	7	2.5	302	2	Q55096	Q55096 synchocyst
809	7	2.5	302	2	Q6SFX4	Q6sfx4 uncultured
810	7	2.5	302	2	Q8D2S4	Q8d2s4 wiggleswort
811	7	2.5	302	2	Q57067	Q57067 hepatitis c
812	7	2.5	303	2	Q74D18	Q74d18 geobacter s
813	7	2.5	303	2	Q7N873	Q7n873 photorhabdu
814	7	2.5	304	2	Q9AQ20	Q9aq20 bradyrhizob
815	7	2.5	304	2	Q82SG0	Q82sg0 nitrosomona
816	7	2.5	304	2	Q83D12	Q83d12 coxiella bu
817	7	2.5	305	2	Q6ML88	Q6ml88 bdellovibri
818	7	2.5	305	2	Q72RE2	Q72re2 leptospira
819	7	2.5	305	2	Q87LU7	Q87lu7 vibrio para
820	7	2.5	305	2	Q8F4C7	Q8f4c7 leptospira
821	7	2.5	305	2	Q9KUD3	Q9kud3 vibrio chol
822	7	2.5	305	2	Q8VIM2	Q8vim2 mus musculus
823	7	2.5	306	2	Q62K72	Q62k72 burkholderi
824	7	2.5	306	2	Q63TX3	Q63tx3 burkholderi
825	7	2.5	306	2	Q98DQ6	Q98dq6 rhizobium l
826	7	2.5	306	2	Q6N432	Q6n432 rhodopsseudo
827	7	2.5	306	2	Q7UJ07	Q7uj07 rhodopirell
828	7	2.5	306	2	Q9S288	Q9s288 streptomyce
829	7	2.5	307	2	Q7MHV1	Q7mhv1 vibrio vuln
830	7	2.5	307	2	Q7VWM9	Q7vwm9 bordetella
831	7	2.5	307	2	Q7WH89	Q7wh89 bordetella
832	7	2.5	307	2	Q89FX1	Q89fx1 bradyrhizob
833	7	2.5	307	2	Q8DC14	Q8dc14 vibrio vuln
834	7	2.5	307	2	Q9HXW8	Q9hwx8 pseudomonas

981 7 2.5 338 2 Q6D122 Q6D122 erwinia car
 982 7 2.5 339 1 F16Q_HUMAN Q00757 homo sapien
 983 7 2.5 339 2 Q976N8 Q976N8 sulfolobus
 984 7 2.5 339 2 Q6F153 Q6F153 homo sapien
 985 7 2.5 339 2 Q9N0J6 Q9N0J6 oryctolagus
 986 7 2.5 339 2 Q8YBT4 Q8YBT4 bruceella me
 987 7 2.5 339 2 Q8YU4 Q8YU4 anabaena sp
 988 7 2.5 339 2 Q9IX26 Q9IX26 mus musculus
 989 7 2.5 339 2 Q9QXD7 Q9QXD7 mus musculus
 990 7 2.5 339 2 Q9Z1N1 Q9Z1N1 rattus norv
 991 7 2.5 340 1 GLS1_YERPE Q9Z49 yersinia pe
 992 7 2.5 340 2 Q8N072 Q8N072 corynebacte
 993 7 2.5 340 2 Q9I9H7 Q9I9H7 zaccocys dhum
 994 7 2.5 341 2 Q7UBN1 Q7UBN1 shigella fl
 995 7 2.5 341 2 Q8XC09 Q8XC09 escherichia
 996 7 2.5 342 2 Q7PU47 Q7PU47 anopheles g
 997 7 2.5 342 2 Q82DR3 Q82DR3 streptomyce
 998 7 2.5 343 1 METN_YERPE Q8zh38 yersinia pe
 999 7 2.5 343 2 Q667L9 Q667L9 yersinia ps
 1000 7 2.5 343 2 Q97NU4 Q97NU4 streptococc

ALIGNMENTS

RESULT 1
 Q97N51 ID Q97N51 PRELIMINARY; PRT; 279 AA.
 AC DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE ABC transporter, ATP-binding protein.
 GN OrderedLocusNames=SP2220;
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC BAA-334 / TIGR4;
 RX MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E.K., Khouri H.M., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T.,
 RA Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
 RL Science 293:498-506(2001).
 CC -!- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AE007509; AAK76268.1; -;
 DR FIR; C95259; C95259.
 DR HSSP; P02915; 1B0U.
 DR TIGR; SP2220; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0042626; P:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 279 AA; 30525 NW; E051E473D082AD32 CRC64;

Query Match 100.0%; Score 279; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 2e-266;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGIALENNVFTYQSGTTLPLAAGLSDVSLTIEDGSYTALIGHTGSGKSTILQLLGLLVPS 60
 DB 1 MGIALENNVFTYQSGTTLPLAAGLSDVSLTIEDGSYTALIGHTGSGKSTILQLLGLLVPS 60
 QY 61 QGSRVVRVDTLITSTSKNDIRQIRKQGLVQFAENQIPETVLKDVAFGQNFVSEED 120
 DB 61 QGSRVVRVDTLITSTSKNDIRQIRKQGLVQFAENQIPETVLKDVAFGQNFVSEED 120
 QY 121 AVKTAREKALVGVDESIFDRSPPELSGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
 DB 121 AVKTAREKALVGVDESIFDRSPPELSGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
 QY 181 RKEMLTFLFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKSPDFQDVVPM 240
 DB 181 RKEMLTFLFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKSPDFQDVVPM 240
 QY 241 EVQLGVPKITAFCKRLADRGVSPKRLPIKIBEPKESLNG 279
 DB 241 EVQLGVPKITAFCKRLADRGVSPKRLPIKIBEPKESLNG 279

RESULT 2

Q8DMY0 ID Q8DMY0 PRELIMINARY; PRT; 279 AA.
 AC DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein ABC-NBP.
 GN Name=ABC-NBP; OrderedLocusNames=spr2025;
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus
 OX NCBI_TaxID=171101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21429245; PubMed=11544234;
 RX DOI=10.1128/JB.183.19.5709-5717.2001;
 RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Bargett S.,
 RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geisinger C.,
 RA Gilmore R., Glass J.S., Kuoja H., Kraft A.R., Lagace R.E.,
 RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
 RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
 RA Norris F.H., O'Garra M., Peery R.B., Robertson G.T., Rocky P.,
 RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
 RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostack P.R. Jr., Skarud P.L.,
 RA Glass J.I.;
 RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
 RL J. Bacteriol. 183:5709-5717(2001).
 CC -!- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AE008566; AAL00827.1; -;
 DR FIR; F98124; F98124.
 DR HSSP; P02915; 1B0U.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0042626; P:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 279 AA; 30553 MW; FBSA148C367A6032 CRC64;

Query Match

59.9%; Score 167; DB 2; Length 279;


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Best Local Similarity 99.6%; Pred. No. 6.8e-156;
Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 YQEGTFLASALSDVSLTIEDSGSYTALIGHTSGKSTILQLLNGLLVPSQGSVRVFDTLI 71
Db 12 YQEGTFLASALSDVSLTIEDSGSYTALIGHTSGKSTILQLLNGLLVPSQGSVRVFDTLI 71
QY 72 TSTSKNKDIQIRKQVGLVQFAENQIPEETVLKDVAFGPQNGFVSEEDAVKTAREKAL 131
Db 72 TSTSKNKDIQIRKQVGLVQFAENQIPEETVLKDVAFGPQNGFVSEEDAVKTAREKAL 131
QY 132 VGIDSLFDRSPFELSGGQRRVATAGILAMEPAILVLDEPTAGLDPLGRKELMTLFLFKL 191
Db 132 VGIDSLFDRSPFELSGGQRRVATAGILAMEPAILVLDEPTAGLDPLGRKELMTLFLFKL 191
QY 192 HQSGMTIVLTHLMDVDAFYANQVYMEKGRVLKGGKPSDVFQDVVFMEVQLGVPKITA 251
Db 192 HQSGMTIVLTHLMDVDAFYANQVYMEKGRVLKGGKPSDVFQDVVFMEVQLGVPKITA 251
QY 252 FCKRLADRGVSKRLPIKIEEKSLSNG 279
Db 252 FCKRLADRGVSKRLPIKIEEKSLSNG 279

RESULT 3
Q9CIS8 PRELIMINARY; PRT; 288 AA.
AC Q9CIS8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter ATP-binding protein.
GN Name=yche; OrderedLocusNames=Li0278;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.1697R;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AF06265; AAK04376.1; --
DR PIR; F8659; F8659.
DR HSSP; P58301; 1US8.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete_proteome.
KW SEQUENCE 288 AA; 31848 MW; 9326C417DE7AEF22 CRC64;
SQ SEQUENCE FROM N.A.
RC STRAIN=11403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.1697R;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AF06265; AAK04376.1; --
DR PIR; F8659; F8659.
DR HSSP; P58301; 1US8.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete_proteome.
KW SEQUENCE 288 AA; 31848 MW; 9326C417DE7AEF22 CRC64;
SQ
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Query Match 8.2%; Score 23; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 SPFELSGGQRRVATAGILAMEP 164
Db 141 SPFELSGGQRRVATAGILAMEP 163
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RESULT 4
Q99X12 PRELIMINARY; PRT; 280 AA.
AC Q99X12;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative ABC transporter (ATP-binding protein).
GN OrderedLocusNames=SPY2194;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192884; PubMed=11296296; DOI=10.1073/pnas.071559398;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE005636; AAK34822.1; --
DR HSSP; O58663; 1G9X.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete_proteome.
KW SEQUENCE 280 AA; 30863 MW; DBE44F6F80C7D5 CRC64;
SQ

Query Match 7.9%; Score 22; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 FKKLHQSGMTIVLTHLMDVDA 209
Db 188 FKKLHQSGMTIVLTHLMDVDA 209

RESULT 5
Q7CWM8 PRELIMINARY; PRT; 280 AA.
AC Q7CWM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative ABC transporter (ATP-binding protein).
GN OrderedLocusNames=spym18_2229;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232;
RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.W., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
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OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MEM316 / Serotype III;
RA MEDLINE=22242508; PubMed=12354221;
RX Glaser P., Rueniok C., Buchrieser C., Chevallier F., Frangeul L.,
RA Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513 (2002).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AL766856; CAD47768.1; --
DR HSSP; P58301; IUS8.
DR Sagaliet; gbs2109; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 31111 MW; 00253EF4A7E5C30B CRC64;

Query Match 7.9%; Score 22; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 PFELSGGQRRVAIAGILAMEP 164
DB 143 PFELSGGQRRVAIAGILAMEP 164
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RESULT 9
ID Q8K5H2 PRELIMINARY; PRT; 280 AA.
AC Q8K5H2; Q79VY7.
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Putative ABC transporter (ATP-binding protein).
GN OrderedLocusNames=SPB1841, SpvM3 1845;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Perkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayaishi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights

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RT into phage evolution.";
RL Genome Res. 13:1042-1055 (2003).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE014172; AAM80452.1; --
DR EMBL; AP005146; BAC84936.1; --
DR HSSP; Q58663; IG9X.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30905 MW; 8E7752BD48834752 CRC64;

Query Match 7.9%; Score 22; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 FKCLHQSGMTIVLVTHLMDDDVA 209
DB 188 FKCLHQSGMTIVLVTHLMDDDVA 209
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|||||

RESULT 10
ID P70970 PRELIMINARY; PRT; 276 AA.
AC P70970; Q797S2.
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein orf5 (YbaE protein).
GN Name=orf5; Synonyms=ybaE; OrderedLocusNames=BSU01460;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168.
RX MEDLINE=97124188; PubMed=8969501;
RA Yasumoto K., Liu H., Jeong S.M., Ohashi Y., Kakinuma S., Tanaka K.,
RA Kawamura F., Yoshikawa H., Takahashi H.;
RT "Sequence analysis of a 50 kb region between spoOH and rrnH on the
RT Bacillus subtilis chromosome.";
RL Microbiology 142:3039-3046 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriell R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot P., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrati E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,

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RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
 RA Rey M., Reynolds S., Rieger M., Rivoita C., Rocha E., Roche B.,
 RA Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
 RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
 RA Shin B.S., Soldo B., Sorokin A., Taccioni E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
 RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
 RA Vassarotti A., Viari A., Wambuit R., Wedler E., Wedler H.,
 RA Westzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
 RA Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT *subtilis*,"
 RL Nature 390:249-256(1997).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; D64126; BAA10984.1; -.
 DR EMBL; Z99104; CAB11922.1; -.
 DR PIR; E69742; E69742.
 DR HSSP; Q58653; IGX.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA-ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_tran; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS0211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome; Hypothetical protein.
 SW SEQUENCE 276 AA; 30578 MW; A5AE1B64360016C9 CRC64;

Query Match 6.8%; Score 19; DB 2; Length 276;
 Best Local Similarity 100.0%; Pred. No. 7.6e-10; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 DRSPFELSGGQRRVAIAG 158
 DB 127 DRSPFELSGGQRRVAIAG 145

RESULT 11
 Q65P76 PRELIMINARY; PRT; 289 AA.
 AC Q65P76;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE YbaE (ABC transporter).
 GN Name=YbaE; ORFNames=BL01022, BL100164;
 OS *Bacillus licheniformis* DSM 13.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=279010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 13;
 RX PubMed=15383718;
 RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
 RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
 RA Ehrenreich A., Gottschalk G.;
 RT "The Complete Genome Sequence of *Bacillus licheniformis* DSM13, an
 RT Organism with Great Industrial Potential,"
 RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14580;
 RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
 RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
 RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
 RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
 RA Berk R.M.;

RT "Complete genome sequence of the industrial bacterium *Bacillus*
 RT *licheniformis* and comparisons with closely related *Bacillus* species,"
 RL Genome Biol. 5:R77-R77(2004).
 DR EMBL; AB017333; AAU39138.1; -.
 DR EMBL; CP000002; AAU21793.1; -.
 SQ SEQUENCE 289 AA; 32364 MW; 31B74C69B46A0AC CRC64;

Query Match 6.8%; Score 19; DB 2; Length 289;
 Best Local Similarity 100.0%; Pred. No. 7.9e-10; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 DRSPFELSGGQRRVAIAG 158
 DB 140 DRSPFELSGGQRRVAIAG 158

RESULT 12
 Q8VNL8 PRELIMINARY; PRT; 177 AA.
 ID Q8VNL8
 AC Q8VNL8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative ABC transporter (Fragment).
 OS *Enterococcus faecium* (Streptococcus faecium).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; *Enterococcus*.
 OX NCBI_TaxID=1352;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22105956; PubMed=12110480; DOI=10.1016/S0928-8244(02)00304-8;
 RA Burnie J.P., Carter T.L., Rigg G.P., Hodgetts S.J., Donohoe M.S.,
 RA Matthews R.C.;
 RT Identification of ABC transporters in vancomycin-resistant
 RT *Enterococcus faecium* as potential targets for antibody therapy.";
 RL FEMS Immunol. Med. Microbiol. 33:179-189(2002).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AJ288868; CAD2181.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR PROSITE; PS0211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding.
 FT NON TER 177
 SQ SEQUENCE 177 AA; 19663 MW; B00F2778F106845F CRC64;

Query Match 6.5%; Score 18; DB 2; Length 177;
 Best Local Similarity 100.0%; Pred. No. 5e-09; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQRRVAIAG 158
 DB 141 RSPFELSGGQRRVAIAG 158

RESULT 13
 Q8V455 PRELIMINARY; PRT; 288 AA.
 ID Q8V455
 AC Q8V455;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Lmo2600 protein.
 GN OrderedLocustNames=lmo2600;
 OS *Listeria monocytogenes*.
 OC Bacteria; Firmicutes; Bacillales; *Listeria*.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;

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RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkāt G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AL591983; CAD00678.1; -.
DR PIR; AH1399; AH1399.
DR ListList; LMO2600; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 288 AA; 31971 MW; 8628839C8CAEDBE0 CRC64;

Query Match 6.5%; Score 18; DB 2; Length 288;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQMRRAIAG 158
DB 141 RSPFELSGGQMRRAIAG 158

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AC Q927N9 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lin2749 protein.
GN OrderedLocusNames=lin2749;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkāt G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AL596173; CAC97975.1; -.
DR PIR; AG1775; AG1775.
DR ListList; LIN2749; -.

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DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 288 AA; 31882 MW; F08B7C8B20AEC3F9 CRC64;

Query Match 6.5%; Score 18; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 7.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQMRRAIAG 158
DB 141 RSPFELSGGQMRRAIAG 158

RESULT 15
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AC Q71WH8 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Cobalt ABC transporter, ATP-binding protein.
GN OrderedLocusNames=LMOF2365_2573;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.P., Raeko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson M.C., Nierman W.C., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlrich G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocytogenes reveal new insights into the core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE017331; AAT05338.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 288 AA; 31957 MW; 892B9C838CAEDF7 CRC64;

Query Match 6.5%; Score 18; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 7.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQMRRAIAG 158
DB 141 RSPFELSGGQMRRAIAG 158

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Search completed: October 28, 2005, 18:14:02
Job time : 221 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 18:17:36 ; Search time 168 Seconds
(without alignments)

694.250 Million cell updates/sec

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Perfect score: 279

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Searched: 1865214 seqs, 418043040 residues

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Total number of hits satisfying chosen parameters: 1865214

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Post-processing: Listing first 1000 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	167	59.9	279	9	US-09-815-242-13440
5	167	59.9	279	15	US-10-282-122A-74238
6	22	7.9	280	15	US-10-282-122A-74298
7	22	7.9	280	15	US-10-282-122A-74821
8	19	6.8	276	15	US-10-369-493-23054
9	18	6.5	180	14	US-10-054-968-2
10	18	6.5	272	15	US-10-282-122A-45314
11	18	6.5	288	15	US-10-282-122A-60478

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6.5	293	15	US-10-282-122A-46693	Sequence 46693, A
6.1	289	9	US-09-815-242-10545	Sequence 10545, A
6.1	289	15	US-10-282-122A-57248	Sequence 57248, A
4.7	282	15	US-10-369-493-17105	Sequence 17105, A
4.7	292	18	US-10-501-282-342	Sequence 342, App
4.7	294	18	US-10-501-282-344	Sequence 344, App
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4.3	288	15	US-10-369-493-22886	Sequence 22886, A
3.9	286	15	US-10-282-122A-71345	Sequence 71345, A
3.9	288	15	US-10-282-122A-53490	Sequence 53490, A
3.9	295	15	US-10-282-122A-53480	Sequence 53480, A
3.9	300	9	US-09-861-451A-24	Sequence 42, Appl
3.9	300	15	US-10-282-122A-52783	Sequence 52783, A
3.9	601	14	US-10-156-761-11587	Sequence 11587, A
3.9	856	15	US-10-094-749-2929	Sequence 2929, Ap
3.9	1418	18	US-10-450-763-32543	Sequence 32543, A
3.9	1583	15	US-10-093-463-198	Sequence 198, App
3.9	1585	16	US-10-343-903-30	Sequence 30, Appl
3.9	1624	13	US-10-090-454-2	Sequence 2, Appl
3.9	1624	14	US-10-005-338B-7	Sequence 7, Appl
3.6	196	9	US-09-795-693-25	Sequence 25, Appl
3.6	196	14	US-10-156-239-25	Sequence 25, Appl
3.6	196	14	US-10-193-485-25	Sequence 25, Appl
3.6	198	9	US-09-795-693-41	Sequence 41, Appl
3.6	198	10	US-09-934-421A-4	Sequence 4, Appl
3.6	198	14	US-10-156-239-28	Sequence 28, Appl
3.6	198	14	US-10-156-239-41	Sequence 41, Appl
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3.6	288	18	US-10-724-972A-6429	Sequence 6429, Ap
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3.6	601	15	US-10-369-493-17187	Sequence 17187, A
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3.6	1547	16	US-10-343-903-12	Sequence 12, Appl
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89	9	3.2	292	15	US-10-369-493-10858	Sequence 10858, A	162	8	2.9	600	14	US-10-156-761-8406	Sequence 8406, App
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91	9	3.2	298	15	US-10-282-122A-53207	Sequence 53207, A	164	8	2.9	608	15	US-10-369-493-18422	Sequence 18422, A
92	9	3.2	302	9	US-09-738-626-6862	Sequence 6862, App	165	8	2.9	624	15	US-10-369-493-16411	Sequence 16411, A
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95	9	3.2	345	16	US-10-696-616-30	Sequence 30, Appl	168	8	2.9	646	16	US-10-872-155-567	Sequence 567, App
96	9	3.2	356	16	US-10-437-963-151133	Sequence 151133, A	169	8	2.9	647	15	US-10-282-122A-55195	Sequence 55195, A
97	9	3.2	357	16	US-10-739-930-5819	Sequence 5819, App	169	8	2.9	650	15	US-10-282-122A-60635	Sequence 60635, A
98	9	3.2	381	16	US-10-425-115-221898	Sequence 221898, A	171	8	2.9	673	15	US-10-369-493-17668	Sequence 17668, A
99	9	3.2	528	14	US-10-156-761-13154	Sequence 13154, A	172	8	2.9	674	15	US-10-369-493-17194	Sequence 17194, A
100	9	3.2	554	15	US-10-369-493-115	Sequence 115, App	173	8	2.9	690	15	US-10-369-493-1927	Sequence 1927, App
101	9	3.2	579	18	US-10-450-763-54609	Sequence 54609, A	174	8	2.9	690	16	US-10-762-596-6	Sequence 6, Appl
102	9	3.2	585	15	US-10-369-493-9100	Sequence 9100, App	175	8	2.9	846	16	US-10-437-963-170558	Sequence 170558, A
103	9	3.2	593	15	US-10-369-493-736	Sequence 736, App	176	8	2.9	1117	15	US-10-369-493-20173	Sequence 20173, A
104	9	3.2	605	15	US-10-369-493-2601	Sequence 2601, App	177	8	2.9	1167	15	US-10-369-493-11829	Sequence 11829, A
105	9	3.2	611	15	US-10-369-493-18316	Sequence 18316, A	178	8	2.9	1177	17	US-10-732-923-3293	Sequence 3293, App
106	9	3.2	800	15	US-10-369-493-8317	Sequence 8317, App	179	8	2.9	1199	15	US-10-369-493-9913	Sequence 9913, App
107	9	3.2	950	15	US-10-282-122A-47285	Sequence 47285, A	180	8	2.9	1511	20	US-11-097-143-2427	Sequence 2427, App
108	9	3.2	1081	15	US-10-369-493-374	Sequence 374, App	181	7	2.9	2580	20	US-11-097-143-25572	Sequence 25572, A
109	9	3.2	1105	15	US-10-369-493-21224	Sequence 21224, A	182	7	2.5	7	14	US-10-054-968-4	Sequence 4, Appl
110	9	3.2	1164	15	US-10-369-493-9770	Sequence 9770, App	183	7	2.5	9	10	US-09-847-670-2	Sequence 2, Appl
111	9	3.2	1175	17	US-10-732-923-3302	Sequence 3302, App	184	7	2.5	9	11	US-09-880-505-102	Sequence 2, Appl
112	9	3.2	1182	15	US-10-282-122A-53445	Sequence 53445, A	185	7	2.5	24	10	US-10-051-643-102	Sequence 102, App
113	8	2.9	76	14	US-10-029-386-30724	Sequence 30724, A	186	7	2.5	24	13	US-10-051-643-102	Sequence 102, App
114	8	2.9	79	15	US-10-424-599-169028	Sequence 169028, A	187	7	2.5	28	9	US-09-921-397-13	Sequence 13, Appl
115	8	2.9	119	15	US-10-369-493-17760	Sequence 17760, A	188	7	2.5	30	15	US-10-296-734-570	Sequence 570, App
116	8	2.9	126	16	US-10-437-963-191474	Sequence 191474, A	189	7	2.5	30	15	US-10-296-734-572	Sequence 572, App
117	8	2.9	202	9	US-09-960-253-184	Sequence 184, App	190	7	2.5	43	18	US-10-724-972A-4588	Sequence 4588, App
118	8	2.9	215	14	US-10-172-399-2	Sequence 2, Appl	191	7	2.5	57	15	US-10-424-599-275055	Sequence 275055, A
119	8	2.9	237	15	US-10-369-493-910	Sequence 910, App	192	7	2.5	58	16	US-10-437-963-118605	Sequence 118605, A
120	8	2.9	243	9	US-09-738-626-4852	Sequence 4852, App	193	7	2.5	57	18	US-10-450-763-31958	Sequence 31958, A
121	8	2.9	243	15	US-10-627-416-368	Sequence 368, App	194	7	2.5	72	17	US-10-926-683-1274	Sequence 1274, App
122	8	2.9	243	16	US-10-322-696-129	Sequence 129, App	195	7	2.5	80	15	US-10-424-599-219745	Sequence 219745, A
123	8	2.9	248	15	US-10-369-493-988	Sequence 988, App	196	7	2.5	89	13	US-10-063-559-2	Sequence 2, Appl
124	8	2.9	255	17	US-10-211-028-47	Sequence 47, Appl	197	7	2.5	92	13	US-10-063-559-2	Sequence 2, Appl
125	8	2.9	264	15	US-10-617-320-3084	Sequence 3084, App	198	7	2.5	92	16	US-10-425-115-301617	Sequence 301617, A
126	8	2.9	274	15	US-10-282-122A-60842	Sequence 60842, A	199	7	2.5	94	17	US-10-732-923-24132	Sequence 24132, A
127	8	2.9	277	16	US-10-437-963-137553	Sequence 137553, A	200	7	2.5	95	16	US-10-425-115-304772	Sequence 304772, A
128	8	2.9	280	14	US-10-156-761-9519	Sequence 9519, App	201	7	2.5	98	16	US-10-425-115-309960	Sequence 309960, A
129	8	2.9	297	15	US-10-369-493-4587	Sequence 4587, App	202	7	2.5	98	17	US-10-926-683-1586	Sequence 1586, App
130	8	2.9	298	15	US-10-369-493-8597	Sequence 8597, App	203	7	2.5	102	9	US-09-767-870-11	Sequence 11, Appl
131	8	2.9	300	15	US-10-369-493-7344	Sequence 7344, App	204	7	2.5	102	14	US-10-242-568-11	Sequence 11, Appl
132	8	2.9	306	15	US-10-369-493-18052	Sequence 18052, A	205	7	2.5	102	16	US-10-425-115-198828	Sequence 198828, A
133	8	2.9	380	15	US-10-369-493-9637	Sequence 9637, App	206	7	2.5	103	15	US-10-424-599-14744	Sequence 14744, A
134	8	2.9	384	15	US-10-369-493-8884	Sequence 8884, App	207	7	2.5	108	17	US-10-391-939A-8	Sequence 8, Appl
135	8	2.9	385	10	US-09-769-787-144	Sequence 144, App	208	7	2.5	109	18	US-10-501-962A-24	Sequence 24, Appl
136	8	2.9	385	17	US-10-472-928-2816	Sequence 2816, App	209	7	2.5	111	16	US-10-767-701-52573	Sequence 52573, A
137	8	2.9	385	18	US-10-617-320-3770	Sequence 3770, App	210	7	2.5	111	17	US-10-926-683-15332	Sequence 15332, App
138	8	2.9	407	16	US-10-425-115-33618	Sequence 33618, A	211	7	2.5	112	16	US-10-437-963-175313	Sequence 175313, A
139	8	2.9	433	18	US-10-501-282-6190	Sequence 6190, App	212	7	2.5	116	18	US-10-450-763-35261	Sequence 35261, A
140	8	2.9	467	15	US-10-424-599-161382	Sequence 161382, A	213	7	2.5	117	16	US-10-437-963-111007	Sequence 111007, A
141	8	2.9	475	14	US-10-076-157-4	Sequence 4, Appl	214	7	2.5	117	16	US-10-767-701-51081	Sequence 51081, A
142	8	2.9	479	15	US-10-369-493-17963	Sequence 17963, A	215	7	2.5	121	16	US-10-403-142-70	Sequence 70, Appl
143	8	2.9	483	16	US-10-425-115-333619	Sequence 333619, A	216	7	2.5	125	14	US-10-189-940-145	Sequence 145, App
144	8	2.9	506	15	US-10-282-122A-76906	Sequence 76906, A	217	7	2.5	125	16	US-10-403-142-66	Sequence 66, Appl
145	8	2.9	511	15	US-10-369-493-10376	Sequence 10376, A	218	7	2.5	125	15	US-10-971-479-145	Sequence 145, App
146	8	2.9	530	18	US-10-501-282-6192	Sequence 6192, App	219	7	2.5	127	15	US-10-094-749-2807	Sequence 2807, App
147	8	2.9	549	15	US-10-282-122A-50157	Sequence 50157, A	220	7	2.5	130	16	US-10-425-115-333951	Sequence 333951, A
148	8	2.9	555	8	US-08-781-986A-5247	Sequence 5247, App	221	7	2.5	131	16	US-10-767-701-33416	Sequence 33416, A
149	8	2.9	555	15	US-10-329-624-5247	Sequence 5247, App	222	7	2.5	133	16	US-10-437-963-112486	Sequence 112486, A
150	8	2.9	560	18	US-10-501-282-3004	Sequence 3004, App	223	7	2.5	133	16	US-10-425-115-274605	Sequence 274605, A
151	8	2.9	561	15	US-10-369-493-9808	Sequence 9808, App	224	7	2.5	142	9	US-09-966-546-22	Sequence 22, Appl
152	8	2.9	567	18	US-10-724-972A-7424	Sequence 7424, App	225	7	2.5	142	9	US-09-966-546-22	Sequence 22, Appl
153	8	2.9	572	18	US-10-501-282-6194	Sequence 6194, App	226	7	2.5	142	10	US-09-965-212-22	Sequence 22, Appl
154	8	2.9	574	18	US-10-501-282-6196	Sequence 6196, App	227	7	2.5	142	14	US-10-189-940-22	Sequence 22, Appl
155	8	2.9	575	15	US-10-369-493-18840	Sequence 18840, A	228	7	2.5	142	14	US-10-189-940-146	Sequence 146, App
156	8	2.9	576	15	US-10-369-493-19977	Sequence 19977, A	229	7	2.5	142	16	US-10-403-142-64	Sequence 64, Appl
157	8	2.9	583	9	US-09-815-242-13458	Sequence 13458, A	230	7	2.5	142	16	US-10-403-142-68	Sequence 68, Appl

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232	7	2.5	142	18	US-10-971-479-146	Sequence 146, App	305	7	2.5	235	17	US-10-732-923-1558	Sequence 1558, Ap
233	7	2.5	143	17	US-10-732-923-24136	Sequence 24136, A	306	7	2.5	237	18	US-10-501-282-6270	Sequence 6270, Ap
234	7	2.5	143	17	US-10-732-923-24137	Sequence 24137, A	307	7	2.5	241	11	US-09-825-423C-6	Sequence 6, Appli
235	7	2.5	145	10	US-09-764-891-3645	Sequence 3645, Ap	308	7	2.5	241	15	US-10-425-114-42421	Sequence 42421, A
236	7	2.5	147	16	US-10-767-701-36763	Sequence 36763, A	309	7	2.5	244	15	US-10-424-599-171724	Sequence 171724, A
237	7	2.5	148	11	US-09-825-423C-3	Sequence 3, Appli	310	7	2.5	246	15	US-10-282-122A-49651	Sequence 49651, A
238	7	2.5	150	17	US-10-889-503-27	Sequence 27, Appl	311	7	2.5	247	14	US-10-156-761-13831	Sequence 13831, A
239	7	2.5	151	16	US-10-772-021-9	Sequence 9, Appli	312	7	2.5	248	14	US-10-156-761-13831	Sequence 6094, Ap
240	7	2.5	152	16	US-10-772-021-7	Sequence 7, Appli	313	7	2.5	249	9	US-09-738-626-6094	Sequence 6272, Ap
241	7	2.5	155	16	US-10-425-115-369032	Sequence 369032, A	314	7	2.5	251	18	US-10-501-282-6272	Sequence 119, App
242	7	2.5	157	13	US-10-071-751-18	Sequence 18, Appl	315	7	2.5	252	9	US-09-860-670-119	Sequence 119, App
243	7	2.5	157	13	US-09-921-397-84	Sequence 84, Appl	316	7	2.5	252	15	US-10-227-646-119	Sequence 45630, A
244	7	2.5	158	16	US-10-767-701-55394	Sequence 55394, A	317	7	2.5	256	16	US-10-767-701-45630	Sequence 30162, A
245	7	2.5	159	17	US-10-889-503-26	Sequence 26, Appl	318	7	2.5	256	16	US-10-425-115-301162	Sequence 301162, A
246	7	2.5	161	17	US-10-889-503-28	Sequence 28, Appl	319	7	2.5	256	16	US-10-425-115-301162	Sequence 301166, A
247	7	2.5	162	9	US-09-795-693-40	Sequence 40, Appl	320	7	2.5	257	20	US-11-097-143-1611	Sequence 1611, Ap
248	7	2.5	162	14	US-10-156-239-40	Sequence 40, Appl	321	7	2.5	258	15	US-10-369-493-18554	Sequence 18554, A
249	7	2.5	162	14	US-10-199-485-40	Sequence 40, Appl	322	7	2.5	260	15	US-10-369-493-5063	Sequence 5063, Ap
250	7	2.5	162	14	US-10-156-761-1786	Sequence 7786, Ap	323	7	2.5	262	14	US-10-156-761-11145	Sequence 11145, A
251	7	2.5	165	16	US-10-425-115-228496	Sequence 228496, Ap	324	7	2.5	263	9	US-09-921-397-85	Sequence 85, Appli
252	7	2.5	166	16	US-10-767-701-61137	Sequence 61137, A	325	7	2.5	263	17	US-10-391-939A-6	Sequence 6, Appli
253	7	2.5	173	16	US-10-425-115-276631	Sequence 276631, A	326	7	2.5	263	17	US-10-391-939A-32	Sequence 32, Appl
254	7	2.5	174	16	US-10-767-701-48755	Sequence 48755, Ap	327	7	2.5	263	17	US-10-391-939A-39	Sequence 39, Appl
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256	7	2.5	176	15	US-10-369-493-10441	Sequence 10441, A	329	7	2.5	264	15	US-10-425-114-57651	Sequence 57651, A
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258	7	2.5	177	16	US-10-425-115-257936	Sequence 257936, A	331	7	2.5	266	20	US-11-126-662-7	Sequence 7, Appli
259	7	2.5	185	9	US-09-529-063-34	Sequence 34, Appl	332	7	2.5	267	15	US-10-461-194-91	Sequence 91, Appl
260	7	2.5	185	14	US-10-414-378-34	Sequence 34, Appl	333	7	2.5	267	15	US-10-461-194-121	Sequence 121, App
261	7	2.5	189	15	US-10-369-493-9540	Sequence 9540, Ap	334	7	2.5	269	15	US-10-282-122A-44154	Sequence 44154, A
262	7	2.5	192	14	US-10-252-819-15	Sequence 15, Appl	335	7	2.5	269	15	US-10-282-122A-71162	Sequence 71162, A
263	7	2.5	192	16	US-10-767-701-62326	Sequence 62326, A	336	7	2.5	269	17	US-10-857-625-741	Sequence 741, App
264	7	2.5	194	9	US-09-921-397-86	Sequence 86, Appl	337	7	2.5	272	10	US-09-884-456-84	Sequence 84, Appl
265	7	2.5	194	15	US-10-425-114-55787	Sequence 55787, A	338	7	2.5	272	15	US-10-884-456-84	Sequence 177737, A
266	7	2.5	194	15	US-10-335-977-5407	Sequence 5407, Ap	339	7	2.5	274	9	US-09-815-242-5549	Sequence 5549, Ap
267	7	2.5	197	15	US-10-369-493-23120	Sequence 23120, A	340	7	2.5	274	15	US-10-282-122A-63496	Sequence 63496, A
268	7	2.5	197	15	US-10-627-476-470	Sequence 470, App	341	7	2.5	274	15	US-10-282-122A-64292	Sequence 64292, A
269	7	2.5	198	15	US-10-424-599-275210	Sequence 275210, A	342	7	2.5	275	14	US-10-156-761-12256	Sequence 12256, A
270	7	2.5	200	15	US-10-424-599-161479	Sequence 161479, A	343	7	2.5	275	17	US-10-732-923-1581	Sequence 1581, Ap
271	7	2.5	202	15	US-10-369-493-19395	Sequence 19395, A	344	7	2.5	276	17	US-10-732-923-1499	Sequence 1499, Ap
272	7	2.5	202	15	US-10-282-122A-48935	Sequence 48935, A	345	7	2.5	277	15	US-10-282-122A-53483	Sequence 53483, A
273	7	2.5	205	14	US-10-169-048-36	Sequence 36, Appl	346	7	2.5	277	15	US-10-651-165-278	Sequence 278, App
274	7	2.5	205	20	US-11-144-352-36	Sequence 36, Appl	347	7	2.5	277	15	US-10-651-165-277	Sequence 277, App
275	7	2.5	207	18	US-10-958-169-2	Sequence 2, Appli	348	7	2.5	278	9	US-09-921-397-83	Sequence 83, Appl
276	7	2.5	208	15	US-10-369-493-17420	Sequence 2, Appli	349	7	2.5	278	15	US-10-282-122A-55379	Sequence 55379, A
277	7	2.5	209	18	US-10-721-922A-110	Sequence 110, App	350	7	2.5	278	15	US-10-651-165-57	Sequence 57, Appl
278	7	2.5	210	16	US-10-425-115-211307	Sequence 211307, A	351	7	2.5	278	15	US-10-651-165-178	Sequence 178, App
279	7	2.5	213	16	US-10-425-115-301161	Sequence 301161, A	352	7	2.5	278	15	US-10-651-165-265	Sequence 265, App
280	7	2.5	215	9	US-09-924-356A-36	Sequence 36, Appl	353	7	2.5	278	15	US-10-651-165-266	Sequence 266, App
281	7	2.5	215	16	US-10-437-963-166562	Sequence 166562, A	354	7	2.5	278	15	US-10-651-165-267	Sequence 267, App
282	7	2.5	215	16	US-10-425-115-251276	Sequence 251276, A	355	7	2.5	278	15	US-10-651-165-268	Sequence 268, App
283	7	2.5	216	16	US-10-425-115-239832	Sequence 239832, A	356	7	2.5	278	15	US-10-651-165-269	Sequence 269, App
284	7	2.5	216	17	US-10-732-923-5834	Sequence 5834, Ap	357	7	2.5	278	15	US-10-651-165-270	Sequence 270, App
285	7	2.5	219	16	US-10-767-701-52070	Sequence 52070, A	358	7	2.5	278	15	US-10-651-165-271	Sequence 271, App
286	7	2.5	220	15	US-10-369-493-9636	Sequence 9626, Ap	359	7	2.5	278	15	US-10-651-165-272	Sequence 272, App
287	7	2.5	221	15	US-10-282-122A-48012	Sequence 48012, A	360	7	2.5	278	15	US-10-651-165-273	Sequence 273, App
288	7	2.5	222	16	US-10-474-776-347	Sequence 347, App	361	7	2.5	278	15	US-10-651-165-274	Sequence 274, App
289	7	2.5	223	9	US-09-738-626-6926	Sequence 6926, Ap	362	7	2.5	278	15	US-10-651-165-275	Sequence 275, App
290	7	2.5	226	16	US-10-437-963-109136	Sequence 109136, A	363	7	2.5	278	15	US-10-651-165-276	Sequence 276, App
291	7	2.5	228	15	US-10-282-122A-65535	Sequence 65535, A	364	7	2.5	278	16	US-10-703-086-2	Sequence 2, Appli
292	7	2.5	228	17	US-10-732-923-24129	Sequence 24129, A	365	7	2.5	278	17	US-10-855-896-2	Sequence 52131, A
293	7	2.5	228	18	US-10-617-320-4063	Sequence 4063, Ap	366	7	2.5	279	15	US-10-282-122A-60654	Sequence 60654, A
294	7	2.5	229	17	US-10-732-923-24131	Sequence 24131, A	367	7	2.5	279	18	US-10-450-763-56216	Sequence 56216, A
295	7	2.5	230	15	US-10-369-493-172	Sequence 172, App	368	7	2.5	279	18	US-10-501-282-346	Sequence 346, App
296	7	2.5	230	16	US-10-425-115-277148	Sequence 277148, A	369	7	2.5	280	18	US-10-724-972A-4419	Sequence 4419, Ap
297	7	2.5	232	15	US-10-369-493-7757	Sequence 7757, Ap	370	7	2.5	281	17	US-10-472-928-3124	Sequence 3124, Ap
298	7	2.5	233	15	US-10-369-493-10533	Sequence 10533, A	371	7	2.5	282	14	US-10-188-012-3	Sequence 3, Appli
299	7	2.5	234	15	US-10-424-599-177736	Sequence 177736, A	372	7	2.5	282	17	US-10-863-497-3	Sequence 3, Appli
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301	7	2.5	235	15	US-10-369-493-19336	Sequence 19336, A	374	7	2.5	284	15	US-10-767-870-17	Sequence 17, Appl
302	7	2.5	235	15	US-10-282-122A-70031	Sequence 70031, A	375	7	2.5	285	9	US-09-767-870-17	Sequence 17, Appl
303	7	2.5	235	15	US-10-282-122A-70117	Sequence 70117, A	376	7	2.5	285	14	US-10-242-568-17	Sequence 17, Appl

377	7	2.5	285	15	US-10-282-122A-52539	Sequence 52539, A	450	7	2.5	311	9	US-09-808-589A-2	Sequence 2, Appli
378	7	2.5	288	11	US-09-825-423C-5	Sequence 5, Appli	451	7	2.5	311	9	US-09-553-874-4	Sequence 4, Appli
379	7	2.5	288	14	US-10-761-761-11595	Sequence 11595, A	452	7	2.5	311	10	US-09-808-898-18	Sequence 18, Appl
380	7	2.5	290	18	US-10-724-972A-6394	Sequence 6394, Ap	453	7	2.5	311	14	US-10-348-074-38	Sequence 38, Appl
381	7	2.5	291	15	US-10-369-493-19624	Sequence 19624, A	454	7	2.5	311	16	US-10-767-701-33503	Sequence 33503, A
382	7	2.5	292	15	US-10-424-599-148108	Sequence 148108, A	455	7	2.5	311	16	US-10-829-432-8	Sequence 8, Appli
383	7	2.5	292	17	US-10-732-923-1510	Sequence 1510, Ap	456	7	2.5	311	17	US-10-472-928-3580	Sequence 3580, Ap
384	7	2.5	293	9	US-09-738-626-4857	Sequence 4857, Ap	457	7	2.5	312	15	US-10-369-493-14590	Sequence 14590, A
385	7	2.5	294	15	US-10-414-219-2	Sequence 2, Appli	458	7	2.5	312	15	US-10-282-122A-77770	Sequence 77770, A
386	7	2.5	294	15	US-10-282-122A-76896	Sequence 76896, A	459	7	2.5	313	17	US-10-732-923-7802	Sequence 7802, Ap
387	7	2.5	295	10	US-09-896-032-2	Sequence 2, Appli	460	7	2.5	314	14	US-10-156-761-13748	Sequence 13748, A
388	7	2.5	295	15	US-10-425-114-45402	Sequence 45402, A	461	7	2.5	314	15	US-10-369-493-17049	Sequence 17049, A
389	7	2.5	295	17	US-10-802-891-2	Sequence 2, Appli	462	7	2.5	314	15	US-10-369-493-18123	Sequence 18123, A
390	7	2.5	296	16	US-10-425-115-363468	Sequence 363468, A	463	7	2.5	314	15	US-10-369-493-20982	Sequence 20982, A
391	7	2.5	297	15	US-10-369-493-9980	Sequence 9980, Ap	464	7	2.5	314	15	US-10-369-493-21622	Sequence 21622, A
392	7	2.5	297	15	US-10-369-493-11552	Sequence 11552, A	465	7	2.5	315	15	US-10-282-122A-60298	Sequence 60298, A
393	7	2.5	298	15	US-10-369-493-16121	Sequence 16121, A	466	7	2.5	315	15	US-10-282-122A-72901	Sequence 72901, A
394	7	2.5	298	15	US-10-369-493-20421	Sequence 20421, A	467	7	2.5	315	18	US-10-617-320-3914	Sequence 3914, Ap
395	7	2.5	298	15	US-10-282-122A-69688	Sequence 69688, A	468	7	2.5	316	15	US-10-369-493-18754	Sequence 18754, A
396	7	2.5	298	15	US-10-424-599-180038	Sequence 180038, A	469	7	2.5	316	15	US-10-369-493-20198	Sequence 20198, A
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398	7	2.5	299	10	US-09-884-456-68	Sequence 68, Appl	471	7	2.5	317	15	US-10-282-122A-71844	Sequence 71844, A
399	7	2.5	299	10	US-09-884-455-66	Sequence 66, Appl	472	7	2.5	319	15	US-10-724-972A-6323	Sequence 6323, Ap
400	7	2.5	299	10	US-09-884-455-68	Sequence 68, Appl	473	7	2.5	322	15	US-10-425-114-68400	Sequence 68400, A
401	7	2.5	299	15	US-10-369-493-13820	Sequence 13820, A	474	7	2.5	323	15	US-10-425-114-54322	Sequence 54322, A
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403	7	2.5	300	15	US-10-369-493-12609	Sequence 12609, A	476	7	2.5	326	15	US-10-282-122A-56065	Sequence 56065, A
404	7	2.5	300	15	US-10-369-493-17941	Sequence 17941, A	477	7	2.5	326	15	US-10-425-114-63180	Sequence 63180, A
405	7	2.5	300	16	US-10-703-086-5	Sequence 5, Appli	478	7	2.5	327	17	US-10-732-923-7822	Sequence 7822, Ap
406	7	2.5	300	17	US-10-855-897-1	Sequence 1, Appli	479	7	2.5	327	17	US-10-732-923-24135	Sequence 24135, A
407	7	2.5	300	17	US-10-855-896-1	Sequence 1, Appli	480	7	2.5	328	15	US-10-282-122A-42941	Sequence 42941, A
408	7	2.5	301	14	US-10-004-633-24	Sequence 24, Appl	481	7	2.5	330	16	US-10-425-115-341382	Sequence 341382, A
409	7	2.5	301	14	US-10-188-012-29	Sequence 29, Appl	482	7	2.5	330	15	US-10-369-493-21298	Sequence 21298, A
410	7	2.5	301	14	US-10-188-012-31	Sequence 31, Appl	483	7	2.5	330	15	US-10-407-920-36	Sequence 36, Appl
411	7	2.5	301	14	US-10-252-131-24	Sequence 24, Appl	484	7	2.5	330	15	US-10-425-114-58483	Sequence 58483, A
412	7	2.5	301	15	US-10-291-265-752	Sequence 752, App	485	7	2.5	330	15	US-10-407-920-36	Sequence 36, Appl
413	7	2.5	301	15	US-10-354-447-4	Sequence 4, Appli	486	7	2.5	331	14	US-10-156-761-13233	Sequence 13233, A
414	7	2.5	301	15	US-10-354-447-6	Sequence 6, Appli	487	7	2.5	333	15	US-10-282-122A-60539	Sequence 60539, A
415	7	2.5	301	15	US-10-264-237-2772	Sequence 2772, Ap	488	7	2.5	334	15	US-10-655-506-7	Sequence 7, Appli
416	7	2.5	301	17	US-10-663-437-29	Sequence 29, Appl	489	7	2.5	334	17	US-10-718-321-7	Sequence 7, Appli
417	7	2.5	301	17	US-10-663-437-31	Sequence 31, Appl	490	7	2.5	334	17	US-10-450-763-56327	Sequence 56327, A
418	7	2.5	301	17	US-10-838-852-24	Sequence 24, Appl	491	7	2.5	336	18	US-10-450-763-56327	Sequence 56327, A
419	7	2.5	301	18	US-10-958-169-13	Sequence 13, Appl	492	7	2.5	338	15	US-10-425-114-58484	Sequence 58484, A
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421	7	2.5	302	15	US-10-369-493-9159	Sequence 9159, Ap	494	7	2.5	339	9	US-09-808-589A-10	Sequence 10, Appl
422	7	2.5	302	17	US-10-369-493-14945	Sequence 14945, A	495	7	2.5	339	9	US-09-808-589A-12	Sequence 12, Appl
423	7	2.5	302	17	US-10-802-891-9	Sequence 9, Appli	496	7	2.5	339	9	US-09-808-589A-14	Sequence 14, Appl
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426	7	2.5	304	15	US-10-369-493-15736	Sequence 15736, A	499	7	2.5	339	17	US-10-391-939A-2	Sequence 2, Appli
427	7	2.5	304	15	US-10-369-493-20414	Sequence 20414, A	500	7	2.5	339	17	US-10-391-939A-28	Sequence 28, Appl
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429	7	2.5	305	17	US-10-663-497-1	Sequence 1, Appli	502	7	2.5	339	17	US-10-732-923-1569	Sequence 1569, Ap
430	7	2.5	306	9	US-09-815-242-12233	Sequence 12233, A	503	7	2.5	339	17	US-10-732-923-1771	Sequence 1771, Ap
431	7	2.5	306	15	US-10-369-493-9090	Sequence 9090, Ap	504	7	2.5	339	17	US-10-732-923-17857	Sequence 17857, A
432	7	2.5	306	15	US-10-369-493-12077	Sequence 12077, A	505	7	2.5	339	17	US-10-732-923-17858	Sequence 17858, A
433	7	2.5	306	20	US-11-097-143-13455	Sequence 13455, A	506	7	2.5	339	17	US-10-732-923-17862	Sequence 17862, A
434	7	2.5	307	15	US-10-282-122A-66526	Sequence 66526, A	507	7	2.5	339	17	US-10-732-923-18006	Sequence 18006, A
435	7	2.5	307	17	US-10-655-506-3	Sequence 3, Appli	508	7	2.5	339	17	US-10-732-923-18007	Sequence 18007, A
436	7	2.5	308	9	US-09-815-242-10212	Sequence 10212, A	509	7	2.5	339	17	US-10-732-923-18023	Sequence 18023, A
437	7	2.5	308	14	US-10-287-274-392	Sequence 392, App	510	7	2.5	339	17	US-10-732-923-24127	Sequence 24127, A
438	7	2.5	308	15	US-10-369-493-252	Sequence 252, App	511	7	2.5	340	9	US-09-738-626-5233	Sequence 5233, Ap
439	7	2.5	308	15	US-10-369-493-705	Sequence 705, App	512	7	2.5	340	17	US-10-732-923-17994	Sequence 17994, A
440	7	2.5	308	15	US-10-369-493-893	Sequence 893, App	513	7	2.5	341	15	US-10-282-122A-42782	Sequence 42782, A
441	7	2.5	308	15	US-10-369-493-7623	Sequence 7623, Ap	514	7	2.5	341	15	US-10-282-122A-59657	Sequence 59657, A
442	7	2.5	308	15	US-10-369-493-12074	Sequence 12074, A	515	7	2.5	342	14	US-10-156-761-12440	Sequence 12440, A
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444	7	2.5	308	15	US-10-282-122A-56603	Sequence 56603, A	517	7	2.5	342	16	US-10-425-115-274627	Sequence 274627, A
445	7	2.5	308	15	US-10-282-122A-75211	Sequence 75211, A	518	7	2.5	342	17	US-10-732-923-24125	Sequence 24125, A
446	7	2.5	308	17	US-10-893-671-69	Sequence 69, Appl	519	7	2.5	343	17	US-10-732-923-24126	Sequence 24126, A
447	7	2.5	309	15	US-10-369-493-4864	Sequence 4864, Ap	520	7	2.5	343	16	US-10-474-776-380	Sequence 380, App
448	7	2.5	309	15	US-10-369-493-15520	Sequence 15520, A	521	7	2.5	343	17	US-10-472-928-3992	Sequence 3992, Ap
449	7	2.5	309	15	US-10-335-977-5408	Sequence 5408, Ap	522	7	2.5	344	14	US-10-173-480-20	Sequence 20, Appl

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7	2.5	344	15	US-10-282-122A-61560	Sequence 61560, A	7	2.5	361	17	US-10-489-740-191
7	2.5	344	15	US-10-282-122A-66172	Sequence 66172, A	7	2.5	364	14	US-10-188-012-25
7	2.5	344	15	US-10-282-122A-69673	Sequence 69673, A	7	2.5	364	14	US-10-188-012-27
7	2.5	344	16	US-10-753-910-20	Sequence 20, Appl	7	2.5	364	14	US-10-173-480-32
7	2.5	345	15	US-10-282-122A-77050	Sequence 77050, A	7	2.5	364	16	US-10-753-910-32
7	2.5	346	14	US-10-156-761-12401	Sequence 12401, A	7	2.5	364	17	US-10-663-497-25
7	2.5	346	14	US-10-156-761-14945	Sequence 14945, A	7	2.5	364	17	US-10-663-497-27
7	2.5	346	16	US-10-739-930-5782	Sequence 5782, Ap	7	2.5	365	14	US-10-188-012-21
7	2.5	346	17	US-10-732-923-24128	Sequence 24128, A	7	2.5	365	14	US-10-663-497-21
7	2.5	347	15	US-10-282-122A-65496	Sequence 65496, A	7	2.5	366	20	US-11-097-143-11478
7	2.5	347	15	US-10-282-122A-65498	Sequence 65498, A	7	2.5	367	14	US-10-753-480-38
7	2.5	347	15	US-10-282-122A-65653	Sequence 65653, A	7	2.5	367	16	US-10-753-910-38
7	2.5	349	14	US-10-173-480-25	Sequence 25, Appl	7	2.5	368	15	US-10-369-493-8643
7	2.5	349	15	US-10-282-122A-63309	Sequence 63309, A	7	2.5	368	15	US-10-231-956A-446
7	2.5	349	16	US-10-753-910-25	Sequence 25, Appl	7	2.5	369	15	US-10-425-114-68688
7	2.5	350	14	US-10-173-480-18	Sequence 18, Appl	7	2.5	370	15	US-10-282-122A-44678
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7	2.5	351	15	US-10-369-493-2631	Sequence 2631, Appl	7	2.5	370	17	US-10-732-923-20670
7	2.5	352	15	US-10-369-493-6139	Sequence 6139, Appl	7	2.5	370	17	US-10-732-923-20677
7	2.5	352	15	US-10-282-122A-51878	Sequence 51878, A	7	2.5	370	17	US-10-732-923-20684
7	2.5	352	17	US-10-732-923-7846	Sequence 7846, Ap	7	2.5	370	17	US-10-732-923-20684
7	2.5	353	14	US-10-128-714-8177	Sequence 8177, Ap	7	2.5	371	15	US-10-369-493-9285
7	2.5	353	16	US-10-437-963-139000	Sequence 139000, A	7	2.5	371	15	US-10-369-493-9527
7	2.5	353	17	US-10-732-923-7671	Sequence 7671, Ap	7	2.5	371	16	US-10-425-115-301160
7	2.5	353	17	US-10-732-923-7675	Sequence 7675, Ap	7	2.5	371	16	US-10-418-861B-40
7	2.5	353	17	US-10-732-923-7689	Sequence 7689, Ap	7	2.5	377	15	US-10-128-714-3177
7	2.5	353	17	US-10-732-923-7691	Sequence 7691, Ap	7	2.5	378	14	US-10-156-761-12593
7	2.5	353	17	US-10-732-923-7721	Sequence 7721, Ap	7	2.5	379	14	US-10-156-761-13673
7	2.5	353	17	US-10-732-923-7742	Sequence 7742, Ap	7	2.5	379	15	US-10-282-122A-45099
7	2.5	353	17	US-10-732-923-7789	Sequence 7789, Ap	7	2.5	379	15	US-10-282-122A-72658
7	2.5	353	17	US-10-732-923-7790	Sequence 7790, Ap	7	2.5	381	15	US-10-080-170-136
7	2.5	353	17	US-10-732-923-7793	Sequence 7793, Ap	7	2.5	383	15	US-10-282-122A-72469
7	2.5	353	17	US-10-732-923-7796	Sequence 7796, Ap	7	2.5	383	16	US-10-080-170-136
7	2.5	353	17	US-10-732-923-7797	Sequence 7797, Ap	7	2.5	383	16	US-10-468-356-136
7	2.5	353	17	US-10-732-923-7798	Sequence 7798, Ap	7	2.5	384	16	US-10-767-701-45995
7	2.5	353	17	US-10-732-923-7806	Sequence 7806, Ap	7	2.5	385	15	US-10-282-122A-67316
7	2.5	353	17	US-10-732-923-7818	Sequence 7818, Ap	7	2.5	391	13	US-10-087-192-567
7	2.5	353	17	US-10-732-923-7876	Sequence 7876, Ap	7	2.5	391	15	US-10-369-493-14363
7	2.5	353	17	US-10-732-923-7922	Sequence 7922, Ap	7	2.5	391	15	US-10-767-701-45470
7	2.5	353	17	US-10-732-923-7965	Sequence 7965, Ap	7	2.5	395	15	US-10-425-114-45405
7	2.5	353	17	US-10-732-923-7966	Sequence 7966, Ap	7	2.5	395	15	US-10-425-114-45405
7	2.5	354	15	US-10-369-493-2800	Sequence 2800, Ap	7	2.5	399	15	US-10-424-599-168219
7	2.5	354	17	US-10-732-923-7690	Sequence 7690, Ap	7	2.5	404	10	US-10-369-493-17559
7	2.5	354	17	US-10-732-923-7718	Sequence 7718, Ap	7	2.5	414	15	US-10-424-599-234379
7	2.5	354	17	US-10-732-923-7718	Sequence 7718, Ap	7	2.5	414	15	US-10-425-114-52749
7	2.5	354	17	US-10-732-923-17859	Sequence 17859, A	7	2.5	414	15	US-10-425-114-54795
7	2.5	355	14	US-10-173-480-40	Sequence 40, Appl	7	2.5	424	14	US-10-407-920-37
7	2.5	355	16	US-10-753-910-40	Sequence 40, Appl	7	2.5	424	15	US-10-424-599-167317
7	2.5	355	17	US-10-732-923-7743	Sequence 7743, Ap	7	2.5	424	16	US-10-425-115-215475
7	2.5	355	17	US-10-732-923-7800	Sequence 7800, Ap	7	2.5	427	15	US-10-369-493-3609
7	2.5	355	17	US-10-732-923-7801	Sequence 7801, Ap	7	2.5	427	15	US-10-369-493-3609
7	2.5	356	17	US-10-732-923-7808	Sequence 7808, Ap	7	2.5	427	15	US-10-282-122A-60634
7	2.5	357	17	US-10-732-923-7847	Sequence 7847, Ap	7	2.5	429	18	US-10-617-320-3815
7	2.5	357	17	US-10-732-923-7847	Sequence 7847, Ap	7	2.5	429	18	US-10-282-122A-49236
7	2.5	358	15	US-10-173-480-36	Sequence 36, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	358	15	US-10-282-122A-52728	Sequence 52728, A	7	2.5	431	15	US-10-282-122A-50037
7	2.5	358	16	US-10-753-910-36	Sequence 36, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	359	14	US-10-188-012-17	Sequence 17, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	359	14	US-10-188-012-19	Sequence 19, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	359	14	US-10-188-012-23	Sequence 23, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	359	15	US-10-295-027-302	Sequence 302, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	359	15	US-10-188-832-64	Sequence 64, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	359	17	US-10-391-939A-4	Sequence 4, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	359	17	US-10-663-497-17	Sequence 17, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	359	17	US-10-663-497-19	Sequence 19, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	359	17	US-10-663-497-23	Sequence 23, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	359	17	US-10-732-923-24134	Sequence 24134, A	7	2.5	431	15	US-10-282-122A-50037
7	2.5	359	17	US-10-718-321-8	Sequence 8, Appl	7	2.5	431	15	US-10-282-122A-50037
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7	2.5	360	15	US-10-425-114-39088	Sequence 39088, A	7	2.5	431	15	US-10-282-122A-50037
7	2.5	361	14	US-10-149-819-10	Sequence 10, Appl	7	2.5	431	15	US-10-282-122A-50037
7	2.5	361	16	US-10-723-860-2223	Sequence 2223, Ap	7	2.5	431	15	US-10-282-122A-50037
7	2.5	361	16	US-10-723-860-2223	Sequence 2223, Ap	7	2.5	431	15	US-10-282-122A-50037

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670	7	2.5	460	15	US-10-369-493-20244	Sequence 20244, A	743	7	2.5	560	15	US-10-369-493-19343	Sequence 19343, A
671	7	2.5	461	16	US-10-425-115-263463	Sequence 263463, A	744	7	2.5	560	16	US-10-474-776-827	Sequence 247, App
672	7	2.5	465	14	US-10-232-643-2	Sequence 2, Appli	745	7	2.5	560	17	US-10-472-928-826	Sequence 826, App
673	7	2.5	467	15	US-10-424-599-230135	Sequence 230135, A	746	7	2.5	561	14	US-10-156-761-13374	Sequence 13374, A
674	7	2.5	470	16	US-10-425-115-327487	Sequence 327487, A	747	7	2.5	562	15	US-10-424-599-251264	Sequence 251264, A
675	7	2.5	473	10	US-09-847-670-1	Sequence 1, Appli	748	7	2.5	564	15	US-10-282-122A-68510	Sequence 68510, A
676	7	2.5	473	11	US-09-847-670-1	Sequence 1, Appli	749	7	2.5	564	15	US-10-282-122A-68510	Sequence 68510, A
677	7	2.5	476	15	US-10-425-114-65097	Sequence 65097, A	750	7	2.5	568	15	US-10-282-122A-74363	Sequence 74363, A
678	7	2.5	478	15	US-10-425-114-44927	Sequence 44927, A	751	7	2.5	571	15	US-10-282-122A-76972	Sequence 76972, A
679	7	2.5	478	15	US-10-425-114-51948	Sequence 51948, A	752	7	2.5	572	15	US-10-369-493-15119	Sequence 15119, A
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681	7	2.5	480	15	US-10-425-114-47349	Sequence 47349, A	754	7	2.5	575	14	US-10-314-657-54	Sequence 54, Appli
682	7	2.5	480	15	US-10-425-114-70221	Sequence 70221, A	755	7	2.5	575	17	US-10-473-193-54	Sequence 54, Appli
683	7	2.5	489	18	US-10-335-977-5328	Sequence 5328, App	756	7	2.5	576	15	US-10-424-599-173221	Sequence 173221, A
684	7	2.5	489	18	US-10-501-282-2614	Sequence 2614, App	757	7	2.5	577	14	US-10-156-761-13213	Sequence 13213, A
685	7	2.5	490	15	US-10-369-493-21753	Sequence 21753, A	758	7	2.5	577	15	US-10-369-493-2917	Sequence 2917, App
686	7	2.5	490	16	US-10-425-115-305707	Sequence 305707, A	759	7	2.5	579	15	US-10-369-493-3014	Sequence 3014, App
687	7	2.5	491	18	US-10-840-060-186	Sequence 186, App	760	7	2.5	580	18	US-10-724-372A-7378	Sequence 7378, App
688	7	2.5	491	18	US-10-840-060-188	Sequence 188, App	761	7	2.5	581	15	US-10-369-493-454	Sequence 454, App
689	7	2.5	491	20	US-11-097-143-1713	Sequence 1713, App	762	7	2.5	581	15	US-10-369-493-9724	Sequence 9724, App
690	7	2.5	491	20	US-11-097-143-27966	Sequence 27966, A	763	7	2.5	581	15	US-10-369-493-19340	Sequence 19340, A
691	7	2.5	492	15	US-10-369-493-2934	Sequence 2934, App	764	7	2.5	582	9	US-09-815-242-10115	Sequence 10115, A
692	7	2.5	492	16	US-10-437-963-204606	Sequence 204606, A	765	7	2.5	582	9	US-09-815-242-14006	Sequence 14006, A
693	7	2.5	493	15	US-10-369-493-13691	Sequence 13691, A	766	7	2.5	582	15	US-10-369-493-784	Sequence 784, App
694	7	2.5	495	15	US-10-369-493-19937	Sequence 19937, A	767	7	2.5	582	15	US-10-369-493-21096	Sequence 21096, A
695	7	2.5	498	15	US-10-369-493-17891	Sequence 17891, A	768	7	2.5	582	15	US-10-282-122A-56502	Sequence 56502, A
696	7	2.5	504	13	US-10-029-180-6	Sequence 6, Appli	769	7	2.5	582	15	US-10-282-122A-59761	Sequence 59761, A
697	7	2.5	504	17	US-10-335-977-5329	Sequence 5329, App	770	7	2.5	582	15	US-10-282-122A-67113	Sequence 67113, A
698	7	2.5	504	17	US-10-952-045-6	Sequence 6, Appli	771	7	2.5	582	15	US-10-282-122A-73088	Sequence 73088, A
699	7	2.5	510	15	US-10-435-114-55765	Sequence 55765, A	772	7	2.5	582	15	US-10-282-122A-75237	Sequence 75237, A
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702	7	2.5	513	16	US-10-474-776-281	Sequence 281, App	775	7	2.5	582	15	US-10-282-122A-78010	Sequence 78010, A
703	7	2.5	513	17	US-10-472-928-1460	Sequence 1460, App	776	7	2.5	583	15	US-10-369-493-20909	Sequence 20909, A
704	7	2.5	513	17	US-10-831-070-226	Sequence 226, App	777	7	2.5	585	15	US-10-369-493-12895	Sequence 12895, A
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706	7	2.5	519	16	US-10-425-115-347839	Sequence 347839, A	779	7	2.5	585	18	US-10-450-763-54656	Sequence 54656, A
707	7	2.5	521	14	US-10-156-761-14809	Sequence 14809, A	780	7	2.5	587	9	US-09-815-242-10960	Sequence 10960, A
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709	7	2.5	522	14	US-10-253-904-49	Sequence 49, Appli	782	7	2.5	587	15	US-10-282-122A-58063	Sequence 58063, A
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711	7	2.5	522	15	US-10-369-493-8482	Sequence 8482, App	784	7	2.5	590	15	US-10-369-493-735	Sequence 735, App
712	7	2.5	522	20	US-11-109-793-49	Sequence 49, Appli	785	7	2.5	590	20	US-11-126-662-3	Sequence 3, Appli
713	7	2.5	523	17	US-10-732-923-24140	Sequence 24140, A	786	7	2.5	592	15	US-10-369-493-7688	Sequence 7688, App
714	7	2.5	524	9	US-09-817-764-2	Sequence 2, Appli	787	7	2.5	593	15	US-10-369-493-2656	Sequence 2656, App
715	7	2.5	524	15	US-10-369-493-23452	Sequence 23452, A	788	7	2.5	598	15	US-10-156-761-9103	Sequence 9103, App
716	7	2.5	525	17	US-10-732-923-8481	Sequence 8481, App	789	7	2.5	598	14	US-10-156-761-9103	Sequence 9103, App
717	7	2.5	526	18	US-10-450-763-58907	Sequence 58907, A	790	7	2.5	599	15	US-10-369-493-17309	Sequence 17309, App
718	7	2.5	529	15	US-10-369-493-10152	Sequence 10152, A	791	7	2.5	600	15	US-10-425-114-70986	Sequence 70986, A
719	7	2.5	529	15	US-10-320-797-3229	Sequence 3229, App	792	7	2.5	600	16	US-10-425-115-318815	Sequence 318815, A
720	7	2.5	530	15	US-10-282-122A-49204	Sequence 49204, A	793	7	2.5	601	15	US-10-369-493-4930	Sequence 4930, App
721	7	2.5	530	15	US-10-282-122A-50228	Sequence 50228, A	794	7	2.5	602	15	US-10-282-122A-51384	Sequence 51384, A
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723	7	2.5	533	15	US-10-282-122A-58817	Sequence 58817, A	796	7	2.5	609	18	US-10-213-974-25	Sequence 25, Appli
724	7	2.5	535	16	US-10-425-115-354711	Sequence 354711, A	797	7	2.5	612	15	US-10-369-493-18046	Sequence 18046, A
725	7	2.5	537	15	US-10-369-493-11425	Sequence 11425, A	798	7	2.5	612	16	US-10-437-963-185375	Sequence 185375, A
726	7	2.5	539	15	US-10-369-493-7862	Sequence 7862, App	799	7	2.5	613	9	US-09-929-955-6	Sequence 6, Appli
727	7	2.5	544	16	US-10-425-115-341467	Sequence 341467, A	800	7	2.5	613	11	US-09-758-759-151	Sequence 151, App
728	7	2.5	546	14	US-10-282-122A-50937	Sequence 50937, A	801	7	2.5	613	13	US-10-104-966-6	Sequence 6, Appli
729	7	2.5	546	14	US-10-156-761-9209	Sequence 9209, App	802	7	2.5	613	15	US-10-369-493-12123	Sequence 12123, A
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731	7	2.5	549	15	US-10-369-493-14647	Sequence 14647, A	804	7	2.5	613	15	US-10-282-122A-75444	Sequence 75444, A
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733	7	2.5	552	16	US-10-425-115-271808	Sequence 271808, A	806	7	2.5	613	16	US-10-817-591-6	Sequence 6, Appli
734	7	2.5	554	9	US-09-738-626-4093	Sequence 4093, App	807	7	2.5	613	20	US-11-021-825-151	Sequence 151, App
735	7	2.5	555	15	US-10-282-122A-47751	Sequence 47751, A	808	7	2.5	614	15	US-10-335-977-8238	Sequence 8238, App
736	7	2.5	555	16	US-10-437-963-139131	Sequence 139131, A	809	7	2.5	615	15	US-10-335-977-8239	Sequence 8239, App
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738	7	2.5	556	15	US-10-369-493-18807	Sequence 18807, A	811	7	2.5	620	14	US-10-156-761-9108	Sequence 9108, App
739	7	2.5	558	16	US-10-437-963-181571	Sequence 181571, A	812	7	2.5	621	15	US-10-369-493-10735	Sequence 10735, A
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741	7	2.5	559	15	US-10-282-122A-49145	Sequence 49145, A	814	7	2.5	625	18	US-10-501-282-3900	Sequence 3900, App

815	7	2.5	627	15	US-10-369-493-12261	Sequence 12261, A	888	7	2.5	686	15	US-10-307-047-5	Sequence 5, Appli
816	7	2.5	628	9	US-09-895-752-20	Sequence 20, Appl	889	7	2.5	686	15	US-10-307-047-6	Sequence 6, Appli
817	7	2.5	628	9	US-09-887-586A-20	Sequence 20, Appl	890	7	2.5	686	15	US-10-307-047-7	Sequence 7, Appli
818	7	2.5	628	9	US-09-903-012-20	Sequence 20, Appl	891	7	2.5	686	15	US-10-307-047-8	Sequence 8, Appli
819	7	2.5	628	10	US-09-900-797-20	Sequence 20, Appl	892	7	2.5	686	15	US-10-307-047-9	Sequence 9, Appli
820	7	2.5	628	11	US-09-893-820-20	Sequence 20, Appl	893	7	2.5	686	15	US-10-307-047-10	Sequence 10, Appl
821	7	2.5	628	13	US-10-041-007-22	Sequence 22, Appl	894	7	2.5	686	15	US-10-307-047-11	Sequence 11, Appl
822	7	2.5	628	14	US-10-025-145A-4	Sequence 4, Appli	895	7	2.5	686	15	US-10-369-493-18725	Sequence 36, Appl
823	7	2.5	631	11	US-09-825-423C-1	Sequence 1, Appli	896	7	2.5	686	15	US-10-637-323-2	Sequence 18725, A
824	7	2.5	631	14	US-10-214-932-78	Sequence 78, Appl	897	7	2.5	686	15	US-10-643-853-3	Sequence 2, Appli
825	7	2.5	631	14	US-10-232-643-1	Sequence 1, Appli	898	7	2.5	686	15	US-10-658-782-2	Sequence 3, Appli
826	7	2.5	632	9	US-09-929-955-29	Sequence 29, Appl	899	7	2.5	686	16	US-10-817-591-17	Sequence 17, Appl
827	7	2.5	632	11	US-09-930-591-12	Sequence 12, Appl	900	7	2.5	686	16	US-10-817-591-31	Sequence 31, Appl
828	7	2.5	632	15	US-10-307-047-12	Sequence 12, Appl	901	7	2.5	686	16	US-10-817-591-32	Sequence 32, Appl
829	7	2.5	632	15	US-10-282-122A-51790	Sequence 51790, A	902	7	2.5	686	16	US-10-817-591-43	Sequence 43, Appl
830	7	2.5	632	16	US-10-817-591-29	Sequence 29, Appl	903	7	2.5	686	16	US-10-817-591-44	Sequence 44, Appl
831	7	2.5	632	20	US-11-043-808-12	Sequence 12, Appl	904	7	2.5	686	16	US-10-817-591-45	Sequence 45, Appl
832	7	2.5	633	9	US-09-815-242-13318	Sequence 13318, A	905	7	2.5	686	16	US-10-817-591-46	Sequence 46, Appl
833	7	2.5	633	10	US-09-769-744A-118	Sequence 118, App	906	7	2.5	686	16	US-10-817-591-47	Sequence 47, Appl
834	7	2.5	633	15	US-10-282-122A-73972	Sequence 73972, A	907	7	2.5	686	16	US-10-817-591-48	Sequence 48, Appl
835	7	2.5	633	17	US-10-472-928-2218	Sequence 2218, Ap	908	7	2.5	686	16	US-10-817-591-49	Sequence 49, Appl
836	7	2.5	634	18	US-10-501-282-3902	Sequence 3902, Ap	909	7	2.5	686	16	US-10-899-715-2	Sequence 2, Appli
837	7	2.5	635	15	US-10-369-493-18399	Sequence 18399, A	910	7	2.5	686	20	US-11-043-808-3	Sequence 3, Appli
838	7	2.5	635	15	US-10-282-122A-74533	Sequence 74533, A	911	7	2.5	686	20	US-11-043-808-4	Sequence 4, Appli
839	7	2.5	635	17	US-10-485-710-123	Sequence 123, App	912	7	2.5	686	20	US-11-043-808-5	Sequence 5, Appli
840	7	2.5	636	15	US-10-282-122A-69527	Sequence 69527, A	913	7	2.5	686	20	US-11-043-808-6	Sequence 6, Appli
841	7	2.5	637	15	US-10-282-122A-72115	Sequence 72115, A	914	7	2.5	686	20	US-11-043-808-7	Sequence 7, Appli
842	7	2.5	639	15	US-10-282-122A-77287	Sequence 77287, A	915	7	2.5	686	20	US-11-043-808-8	Sequence 8, Appli
843	7	2.5	640	17	US-10-732-923-7094	Sequence 7094, Ap	916	7	2.5	686	20	US-11-043-808-9	Sequence 9, Appli
844	7	2.5	642	15	US-10-282-122A-52476	Sequence 52476, A	917	7	2.5	686	20	US-11-043-808-10	Sequence 10, Appl
845	7	2.5	645	15	US-10-369-493-12296	Sequence 12296, A	918	7	2.5	686	20	US-11-043-808-11	Sequence 11, Appl
846	7	2.5	645	15	US-10-282-122A-49713	Sequence 49713, A	919	7	2.5	686	20	US-11-043-808-35	Sequence 36, Appl
847	7	2.5	647	15	US-10-369-493-4710	Sequence 4710, Ap	920	7	2.5	686	20	US-11-043-808-36	Sequence 283633, A
848	7	2.5	647	15	US-10-369-493-7469	Sequence 7469, Ap	921	7	2.5	692	16	US-10-425-115-283633	Sequence 7773, Ap
849	7	2.5	649	15	US-10-282-122A-47858	Sequence 47858, A	922	7	2.5	692	16	US-10-739-930-7773	Sequence 9811, Ap
850	7	2.5	650	18	US-10-617-320-3849	Sequence 3849, Ap	923	7	2.5	693	15	US-10-369-493-9811	Sequence 22333, A
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852	7	2.5	660	9	US-09-815-242-13248	Sequence 13248, A	925	7	2.5	695	15	US-10-335-977-9151	Sequence 9151, Ap
853	7	2.5	660	15	US-10-282-122A-50692	Sequence 50692, A	926	7	2.5	702	15	US-10-437-963-145638	Sequence 145638, A
854	7	2.5	664	18	US-10-617-320-3490	Sequence 3490, Ap	927	7	2.5	706	16	US-10-425-115-368831	Sequence 368831, A
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857	7	2.5	683	16	US-10-425-115-324473	Sequence 324473, A	930	7	2.5	710	15	US-10-424-599-212940	Sequence 184000, A
858	7	2.5	683	17	US-10-500-530-28	Sequence 28, Appl	931	7	2.5	711	16	US-10-437-963-184000	Sequence 1508, Ap
859	7	2.5	685	15	US-10-369-493-12820	Sequence 12820, A	932	7	2.5	712	15	US-10-369-493-1508	Sequence 3977, Ap
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861	7	2.5	686	9	US-09-929-955-17	Sequence 17, Appl	934	7	2.5	713	15	US-10-424-599-227130	Sequence 7770, Ap
862	7	2.5	686	9	US-09-929-955-31	Sequence 31, Appl	935	7	2.5	713	15	US-10-369-493-7770	Sequence 1, Appli
863	7	2.5	686	9	US-09-929-955-32	Sequence 32, Appl	936	7	2.5	728	15	US-10-643-853-1	Sequence 1, Appli
864	7	2.5	686	9	US-09-929-955-43	Sequence 43, Appl	937	7	2.5	728	15	US-10-369-493-6626	Sequence 6626, Ap
865	7	2.5	686	9	US-09-929-955-44	Sequence 44, Appl	938	7	2.5	733	15	US-10-369-493-22251	Sequence 22251, A
866	7	2.5	686	9	US-09-929-955-45	Sequence 45, Appl	939	7	2.5	735	15	US-10-369-493-7908	Sequence 7908, Ap
867	7	2.5	686	9	US-09-929-955-46	Sequence 46, Appl	940	7	2.5	744	15	US-10-762-596-2	Sequence 2, Appli
868	7	2.5	686	9	US-09-929-955-47	Sequence 47, Appl	941	7	2.5	747	16	US-10-762-596-4	Sequence 4, Appli
869	7	2.5	686	9	US-09-929-955-48	Sequence 48, Appl	942	7	2.5	747	16	US-11-097-143-2508	Sequence 2508, Ap
870	7	2.5	686	9	US-09-929-955-49	Sequence 49, Appl	943	7	2.5	761	20	US-10-108-260A-3088	Sequence 3088, Ap
871	7	2.5	686	9	US-09-881-654-2	Sequence 2, Appli	944	7	2.5	766	15	US-10-732-923-1507	Sequence 1507, Ap
872	7	2.5	686	9	US-09-881-239-3	Sequence 3, Appli	945	7	2.5	771	17	US-10-732-923-1507	Sequence 1406, Ap
873	7	2.5	686	10	US-09-884-456-70	Sequence 70, Appl	946	7	2.5	780	9	US-10-437-963-142628	Sequence 142628, A
874	7	2.5	686	10	US-09-884-455-70	Sequence 70, Appl	947	7	2.5	784	16	US-10-335-977-9152	Sequence 9152, Ap
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876	7	2.5	686	11	US-09-930-591-3	Sequence 3, Appli	949	7	2.5	787	15	US-10-369-493-2091	Sequence 2844, Ap
877	7	2.5	686	11	US-09-930-591-4	Sequence 4, Appli	950	7	2.5	789	15	US-10-369-493-2844	Sequence 1507, Ap
878	7	2.5	686	11	US-09-930-591-5	Sequence 5, Appli	951	7	2.5	790	15	US-10-369-493-2844	Sequence 1507, Ap
879	7	2.5	686	11	US-09-930-591-6	Sequence 6, Appli	952	7	2.5	790	14	US-10-156-761-9635	Sequence 9635, Ap
880	7	2.5	686	11	US-09-930-591-7	Sequence 7, Appli	953	7	2.5	791	17	US-10-732-923-8523	Sequence 8523, Ap
881	7	2.5	686	11	US-09-930-591-8	Sequence 8, Appli	954	7	2.5	795	14	US-10-335-977-9153	Sequence 9153, Ap
882	7	2.5	686	11	US-09-930-591-9	Sequence 9, Appli	955	7	2.5	796	17	US-10-369-493-1485	Sequence 1485, Ap
883	7	2.5	686	11	US-09-930-591-10	Sequence 10, Appl	956	7	2.5	797	15	US-10-282-122A-74782	Sequence 74782, A
884	7	2.5	686	11	US-09-930-591-11	Sequence 11, Appl	957	7	2.5	798	15	US-10-732-923-1565	Sequence 1565, Ap
885	7	2.5	686	15	US-10-307-047-2	Sequence 2, Appli	958	7	2.5	805	15	US-09-881-239-5	Sequence 5, Appli
886	7	2.5	686	15	US-10-307-047-3	Sequence 3, Appli	959	7	2.5	821	17	US-09-881-239-5	Sequence 5, Appli
887	7	2.5	686	15	US-10-307-047-4	Sequence 4, Appli	960	7	2.5	829	9	US-09-881-239-5	Sequence 5, Appli

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961 7 2.5 829 15 US-10-643-853-5
962 7 2.5 829 16 US-10-658-782-4
963 7 2.5 831 15 US-10-369-493-17055
964 7 2.5 841 10 US-09-884-456-86
965 7 2.5 841 10 US-09-884-455-86
966 7 2.5 843 15 US-10-369-493-3940
967 7 2.5 843 15 US-10-276-774-1780
968 7 2.5 865 16 US-10-771-931-43
969 7 2.5 923 15 US-10-424-599-275214
970 7 2.5 924 15 US-10-369-493-19654
971 7 2.5 932 15 US-10-425-114-49140
972 7 2.5 942 16 US-10-437-963-198719
973 7 2.5 945 9 US-09-812-350-3
974 7 2.5 945 17 US-10-732-923-7090
975 7 2.5 976 20 US-11-097-143-18735
976 7 2.5 1011 15 US-10-276-774-2143
977 7 2.5 1019 15 US-10-369-493-5042
978 7 2.5 1039 20 US-11-097-143-16164
979 7 2.5 1056 15 US-10-369-493-9664
980 7 2.5 1058 15 US-10-424-599-224979
981 7 2.5 1070 15 US-10-424-599-206083
982 7 2.5 1082 15 US-10-369-493-18815
983 7 2.5 1088 15 US-10-369-493-9742
984 7 2.5 1095 15 US-10-369-493-4059
985 7 2.5 1099 9 US-09-881-654-4
986 7 2.5 1099 15 US-10-637-323-4
987 7 2.5 1099 16 US-10-658-782-6
988 7 2.5 1099 16 US-10-899-715-4
989 7 2.5 1120 16 US-10-437-963-114069
990 7 2.5 1147 15 US-10-429-160-6
991 7 2.5 1147 17 US-10-848-723-2
992 7 2.5 1147 17 US-10-848-723-4
993 7 2.5 1147 17 US-10-848-723-6
994 7 2.5 1147 17 US-10-848-723-8
995 7 2.5 1184 16 US-10-437-963-198716
996 7 2.5 1186 15 US-10-369-493-8116
997 7 2.5 1186 16 US-10-437-963-114070
998 7 2.5 1195 16 US-10-437-963-114070
999 7 2.5 1198 15 US-10-425-114-72712
1000 7 2.5 1210 17 US-10-939-958-1
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ALIGNMENTS

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RESULT 1
US-09-769-744A-26
; Sequence 26, Application US/09769744A
; Publication No. US20030134407A1
; GENERAL INFORMATION:
; APPLICANT: Le Page, Richard WF
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hanniffy, Sean B
; APPLICANT: Hanabro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21122WO
; CURRENT APPLICATION NUMBER: US/09/769,744A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/GB99/02452
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: GB 9816336.3
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/125329
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-744A-26
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Query Match 100.0%; Score 279; DB 10; Length 279;

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Best Local Similarity 100.0%; Pred. No. 2e-259;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIALENNFTYQEGTPLASAALSDVSLTIEDGSGYTAIIGHGTGKSTILQLLNGLLVPS 60
DB 1 MGIALENNFTYQEGTPLASAALSDVSLTIEDGSGYTAIIGHGTGKSTILQLLNGLLVPS 60
QY 61 QGSRVVPDTLITSTSKNKDIRQIRKQVGLVFPQPAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 QGSRVVPDTLITSTSKNKDIRQIRKQVGLVFPQPAENQIFETVLKDVAFQPNFGVSEED 120
QY 121 AVKTAREKIALVGDIDSLFDRSPPELSCGQRRVAIAGILAMEPAAILVLDDEPTAGLDPLG 180
DB 121 AVKTAREKIALVGDIDSLFDRSPPELSCGQRRVAIAGILAMEPAAILVLDDEPTAGLDPLG 180
QY 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVVPME 240
DB 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVVPME 240
QY 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKEKSLNG 279
DB 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKEKSLNG 279
RESULT 2
US-10-472-928-4660
; Sequence 4660, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926WO
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4660
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: ABC transporter, ATP-binding protein
; OTHER INFORMATION: Cellular location: membrane
; OTHER INFORMATION: Similar to strain R6 sequence 15904066 (e-154)
US-10-472-928-4660
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Query Match 100.0%; Score 279; DB 17; Length 279;
Best Local Similarity 100.0%; Pred. No. 2e-259;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIALENNFTYQEGTPLASAALSDVSLTIEDGSGYTAIIGHGTGKSTILQLLNGLLVPS 60
DB 1 MGIALENNFTYQEGTPLASAALSDVSLTIEDGSGYTAIIGHGTGKSTILQLLNGLLVPS 60
QY 61 QGSRVVPDTLITSTSKNKDIRQIRKQVGLVFPQPAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 QGSRVVPDTLITSTSKNKDIRQIRKQVGLVFPQPAENQIFETVLKDVAFQPNFGVSEED 120
QY 121 AVKTAREKIALVGDIDSLFDRSPPELSCGQRRVAIAGILAMEPAAILVLDDEPTAGLDPLG 180
DB 121 AVKTAREKIALVGDIDSLFDRSPPELSCGQRRVAIAGILAMEPAAILVLDDEPTAGLDPLG 180
QY 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVVPME 240
DB 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVVPME 240
QY 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKEKSLNG 279
DB 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKEKSLNG 279
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US-10-617-320-4838	
; Sequence 4838, Application US/10617320	
; Publication No. US20050136404A1	
GENERAL INFORMATION:	
APPLICANT: Lynn A Doucette-Stamm and David Bueh	
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID	
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE	
THERAPEUTICS	
FOR DIAGN	
NUMBER OF SEQUENCES: 5206	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: GENOME THERAPEUTICS CORPORATION	
STREET: 100 Beaver Street	
CITY: Waltham	
STATE: Massachusetts	
COUNTRY: USA	
ZIP: 02354	
COMPUTER READABLE FORM:	
MEDIUM TYPE: CD/ROM ISO9660	
COMPUTER: <Unknown>	
OPERATING SYSTEM: <Unknown>	
SOFTWARE: <Unknown>	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/10/617,320	
FILING DATE: 10-Jul-2003	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: US/09/107,433	
FILING DATE: 30-Jun-1998	
APPLICATION NUMBER: 60/ 085131	
FILING DATE: May 12, 1998	
APPLICATION NUMBER: 60/051553	
FILING DATE: July 2, 1997	
ATTORNEY/AGENT INFORMATION:	
NAME: Ariniello, Pamela Deneke	
REGISTRATION NUMBER: 40,489	
REFERENCE/DOCKET NUMBER: GTC-011	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: (781)893-5007	
TELEFAX: (781)893-8277	
INFORMATION FOR SEQ ID NO: 4838:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 280 amino acids	
TYPE: amino acid	
TOPOLOGY: linear	
MOLECULE TYPE: protein	
HYPOTHETICAL: YES	
ORIGINAL SOURCE:	
ORGANISM: Streptococcus pneumoniae	
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (B) LOCATION 1...280	
SEQUENCE DESCRIPTION: SEQ ID NO: 4838:	
US-10-617-320-4838	
Query Match 95.7%; Score 267; DB 18; Length 280;	
Best Local Similarity 100.0%; Pred. No. 6.7e-248;	
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MGTALENVNFYQSGTPLASAAALSDVSLTTIEDGSGYTLALIGHTGSGKSTILQLLNGLLVPS 60
Db	2 MGTALENVNFYQSGTPLASAAALSDVSLTTIEDGSGYTLALIGHTGSGKSTILQLLNGLLVPS 61
Qy	61 QGSRVRFDTLITSTSKNKDIRQIRKQVGLVFQFAENQIFETVLKDVAFQPNFGVSEED 120
Db	62 QGSRVRFDTLITSTSKNKDIRQIRKQVGLVFQFAENQIFETVLKDVAFQPNFGVSEED 121
Qy	121 AVKTAREKALVGTDESIFDRSPPELGGQMRRAIAGILAMEPAIILVLDPEPTAGLDPLG 180
Db	122 AVKTAREKALVGTDESIFDRSPPELGGQMRRAIAGILAMEPAIILVLDPEPTAGLDPLG 181
Qy	181 RKELMTLTKKLGHSQGMTIVLVTHLMDDDVAEYANQVYVMEKRLVKGKPSDVFQDVVFME 240
US-09-815-242-13440	
; Sequence 13440, Application US/09815242	
; Patent No. US20020061569A1	
GENERAL INFORMATION:	
APPLICANT: Haselbeck, Robert	
APPLICANT: Ohlsen, Kari L.	
APPLICANT: Zyskind, Judith W.	
APPLICANT: Wall, Daniel	
APPLICANT: Trawick, John D.	
APPLICANT: Carr, Grant J.	
APPLICANT: Yamamoto, Robert T.	
APPLICANT: Xu, H. Howard	
TITLE OF INVENTION: Identification of Essential Genes in	
FILE OF INVENTION: Prokaryotes	
FILE REFERENCE: ELITRA.011A	
CURRENT APPLICATION NUMBER: US/09/815,242	
CURRENT FILING DATE: 2001-03-21	
PRIOR APPLICATION NUMBER: 60/191,078	
PRIOR FILING DATE: 2000-03-21	
PRIOR APPLICATION NUMBER: 60/206,848	
PRIOR FILING DATE: 2000-05-23	
PRIOR APPLICATION NUMBER: 60/207,727	
PRIOR FILING DATE: 2000-05-26	
PRIOR APPLICATION NUMBER: 60/242,578	
PRIOR FILING DATE: 2000-10-23	
PRIOR APPLICATION NUMBER: 60/253,625	
PRIOR FILING DATE: 2000-11-27	
PRIOR APPLICATION NUMBER: 60/257,931	
PRIOR FILING DATE: 2000-12-22	
PRIOR APPLICATION NUMBER: 60/269,308	
PRIOR FILING DATE: 2001-02-16	
NUMBER OF SEQ ID NOS: 14110	
SOFTWARE: FastSeq for Windows Version 4.0	
SEQ ID NO 13440	
LENGTH: 279	
TYPE: PRT	
ORGANISM: Streptococcus pneumoniae	
US-09-815-242-13440	
Query Match 59.9%; Score 167; DB 9; Length 279;	
Best Local Similarity 99.6%; Pred. No. 9.1e-152;	
Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	12 YQSGTPLASAAALSDVSLTTIEDGSGYTLALIGHTGSGKSTILQLLNGLLVPSQGSVRVFDTLI 71
Db	12 YQSGTPLASAAALSDVSLTTIEDGSGYTLALIGHTGSGKSTILQLLNGLLVPSQGSVRVFDTLI 71
Qy	72 TSTSKNKDIRQIRKQVGLVFQFAENQIFETVLKDVAFQPNFGVSEEDAVKTAREKAL 131
Db	72 TSTSKNKDIRQIRKQVGLVFQFAENQIFETVLKDVAFQPNFGVSEEDAVKTAREKAL 131
Qy	132 VGIDESLFDSPPELGGQMRRAIAGILAMEPAIILVLDPEPTAGLDPLGRKELMTLTKKL 191
Db	132 VGIDESLFDSPPELGGQMRRAIAGILAMEPAIILVLDPEPTAGLDPLGRKELMTLTKKL 191
Qy	192 HQSGMTIVLVTHLMDDDVAEYANQVYVMEKRLVKGKPSDVFQDVVFMEVQLGVPKITA 251
Db	192 HQSGMTIVLVTHLMDDDVAEYANQVYVMEKRLVKGKPSDVFQDVVFMEVQLGVPKITA 251
Qy	252 FCRLADRGVSFKRLPIKIEEFKESLNG 279
Db	252 FCRLADRGVSFKRLPIKIEEFKESLNG 279
RESULT 5	


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US-10-282-122A-74238
; Sequence 74238, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74238
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-282-122A-74238

Query Match      59.9%; Score 167; DB 15; Length 279;
Best Local Similarity 99.6%; Pred. No. 9.1e-152;
Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 YGEGTPLASAAALSDVSLTIEDGYSYALIGHTSGKSTILQLLGLLVPSQGSVRVFDTLI 71
Db 12 YGEGTPLASAAALSDVSLTIEDGYSYALIGHTSGKSTILQLLGLLVPSQGSVRVFDTLI 71
QY 72 TSTSKNKDIRKQKQVGLVFPFAENQIFETVLKDVAFQFQNGFVSEDAVKTAREKLA 131
Db 72 TSTSKNKDIRKQKQVGLVFPFAENQIFETVLKDVAFQFQNGFVSEDAVKTAREKLA 131
QY 132 VQIDESLFRSPFELSGGQRRVATAGILAMPAILVLDDEPTAGLDPLGRKELMTLTKL 191
Db 132 VQIDESLFRSPFELSGGQRRVATAGILAMPAILVLDDEPTAGLDPLGRKELMTLTKL 191
QY 192 HOSGMTIVLVTHLMDVAVYANQVYVMEKGRVKGKPSDVFQDVVFMEVQVGPKITA 251
Db 192 HOSGMTIVLVTHLMDVAVYANQVYVMEKGRVKGKPSDVFQDVVFMEVQVGPKITA 251
QY 252 FCKRLADRGVSKRLPIKIEEFKESLNG 279
Db 252 FCKRLADRGVSKRLPIKIEEFKESLNG 279
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RESULT 6
US-10-282-122A-72498
; Sequence 72498, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72498
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-282-122A-72498

Query Match      7.9%; Score 22; DB 15; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 PPELGGQRRRVATAGILAMEP 164
Db 143 PPELGGQRRRVATAGILAMEP 164

RESULT 7
US-10-282-122A-74821
; Sequence 74821, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
```


APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 74821
LENGTH: 280
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-10-282-122A-74821
Query Match 7.9%; Score 22; DB 15; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 188 FKXHQSGMTIVLVTHLMDVA 209
DB 188 FKXHQSGMTIVLVTHLMDVA 209
RESULT 8
US-10-369-493-23054
Sequence 23054, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23054
LENGTH: 276
TYPE: PRT
ORGANISM: Bacillus subtilis
US-10-369-493-23054
Query Match 6.8%; Score 19; DB 15; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 DRSPFELSGGQMRRAIAG 158
DB 127 DRSPFELSGGQMRRAIAG 145
RESULT 9
US-10-054-968-2
Sequence 2, Application US/10054968
Publication No. US20030119101A1
GENERAL INFORMATION:
APPLICANT: NEUTEC PHARMA PLC
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF INFECTIONS OF GRAM
TITLE OF INVENTION: POSITIVE
TITLE OF INVENTION: COCCI
FILE REFERENCE: PM 259204
CURRENT APPLICATION NUMBER: US/10/054,968
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US/09/214,307
PRIOR FILING DATE: 1999-01-04
PRIOR APPLICATION NUMBER: PCT/GB97/01830
PRIOR FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: GB9614274.0
PRIOR FILING DATE: 1996-07-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 180
TYPE: PRT
ORGANISM: Enterococcus faecium
US-10-054-968-2
Query Match 6.5%; Score 18; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 141 RSPFELSGGQMRRAIAG 158
DB 145 RSPFELSGGQMRRAIAG 162
RESULT 10
US-10-282-122A-45314
Sequence 45314, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578

```
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 45314
/ LENGTH: 272
/ TYPE: PRT
/ ORGANISM: Bacillus anthracis
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (6)..(6)
/ OTHER INFORMATION: X=any amino acid
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (24)..(24)
/ OTHER INFORMATION: X=any amino acid
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (39)..(39)
/ OTHER INFORMATION: X=any amino acid
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (43)..(43)
/ OTHER INFORMATION: X=any amino acid
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (124)..(124)
/ OTHER INFORMATION: X=any amino acid
US-10-282-122A-45314
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Query Match          6.5%; Score 18; DB 15; Length 272;
Best Local Similarity 100.0%; Pred.No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 141 RSPFELSGQMRRVAIAG 158
DB 133 RSPFELSGQMRRVAIAG 150
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RESULT 11
US-10-282-122A-60478
/ Sequence 60478, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
```

```
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 60478
/ LENGTH: 288
/ TYPE: PRT
/ ORGANISM: Listeria monocytogenes
US-10-282-122A-60478
```

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Query Match          6.5%; Score 18; DB 15; Length 288;
Best Local Similarity 100.0%; Pred.No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 141 RSPFELSGQMRRVAIAG 158
DB 141 RSPFELSGQMRRVAIAG 158
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RESULT 12
US-10-282-122A-57659
/ Sequence 57659, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
```

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; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57659
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57659

Query Match      6.5%; Score 18; DB 15; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      141 RSPFELSGGQMRVAIAG 158
      |||||||
Db      141 RSPFELSGGQMRVAIAG 158
      |||||||

RESULT 14
US-09-815-242-10545
; Sequence 10545, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10545
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10545

Query Match      6.1%; Score 17; DB 9; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      142 SPFELSGGQMRVAIAG 158
      |||||||
Db      142 SPFELSGGQMRVAIAG 158
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RESULT 15
US-10-282-122A-57248
; Sequence 57248, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A

Query Match      6.5%; Score 18; DB 15; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      141 RSPFELSGGQMRVAIAG 158
      |||||||
Db      141 RSPFELSGGQMRVAIAG 158
      |||||||

RESULT 13
US-10-282-122A-46693
; Sequence 46693, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46693
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46693

Query Match      6.5%; Score 18; DB 15; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 57248
/ LENGTH: 289
/ TYPE: PRT
/ ORGANISM: Enterococcus faecalis
US-10-282-122A-57248

Query Match      6.1%; Score 17; DB 15; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      142 SPFELSGGQMRRAIAG 158
Db      142 SPFELSGGQMRRAIAG 158
|||||
|||||

Search completed: October 28, 2005, 18:31:53
Job time : 188 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2005, 17:07:43 ; Search time 170 Seconds
(without alignments)
634.742 Million cell updates/sec

Title: US-09-769-744D-26
Perfect score: 1387
Sequence: 1 MGIALENVNFYQEGTFLAS.....GVSPKRLPIKIEFPKESLNG 279

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq.16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1387	100.0	279	3 AAY81709	Streptococcus
2	1387	100.0	279	6 ABU2751	S. pneumo
3	1386	99.9	279	4 AAM01016	Adk47865 Streptoco
4	1386	99.9	279	8 ADR96203	Novel S.
5	1386	99.9	280	8 ADR96203	Novel S.
6	1378	99.4	279	4 AAU37847	Streptoco
7	1378	99.4	279	6 ABU46314	Protein e
8	1002.5	72.3	280	6 ABU44574	Protein e
9	971	70.0	280	5 ABP26998	Streptoco
10	971	70.0	280	6 ABU46897	Protein e
11	948	68.3	280	5 ABP26997	Streptoco
12	948	68.3	280	8 ADK99875	Streptoco
13	943	68.0	279	8 ADK99877	Streptoco
14	943	68.0	279	8 ADK99878	Streptoco
15	943	68.0	279	8 ADK99876	Streptoco
16	943	68.0	279	8 ADK99883	Streptoco
17	943	68.0	279	8 ADK99885	Streptoco
18	943	68.0	279	8 ADK99879	Streptoco
19	943	68.0	279	8 ADK99884	Streptoco
20	940	67.8	279	8 ADK99880	Streptoco
21	940	67.8	279	8 ADK99881	Streptoco
22	940	67.8	279	8 ADK99882	Streptoco
23	899.5	64.9	288	5 ABB53584	Lactococ
24	850.5	61.3	289	4 AAU34952	Enterococ
25	850.5	61.3	289	6 ABU29324	Protein e

26	845.5	61.0	289	6 ABU29735	Protein e
27	844.5	60.9	316	7 ADH86847	Enterococ
28	836.5	60.3	284	7 ADC96403	E. faeciu
29	794	57.2	292	6 ADB06402	Alloioioc
30	794	57.2	294	6 ADB06404	Alloioioc
31	729	52.6	276	8 ADS44624	Bacterial
32	700	50.5	293	6 ABU18769	Protein e
33	692.5	49.9	288	5 ABB47921	Listeria
34	692.5	49.9	288	6 ABU32554	Protein e
35	683	49.2	286	6 ABU24072	Protein e
36	661	47.7	288	6 ABU24767	Protein e
37	637.5	46.0	282	8 ADS28072	Bacterial
38	635.5	45.8	288	6 ABU25566	Protein e
39	611	44.1	286	6 ABU43237	Protein e
40	608	43.8	288	5 ABP38447	Staphyloc
41	608	43.8	288	8 ADS07134	Staphyloc
42	607	43.8	286	6 ABU43421	Protein e
43	594.5	42.9	286	4 AAU36641	Staphyloc
44	589.5	42.5	286	6 ABU16471	Protein e
45	589.5	42.5	286	6 ABM73355	Staphyloc

ALIGNMENTS

RESULT 1

AAV81709
ID AAY81709 standard; protein; 279 AA.

XX
AC AAY81709;

DT
XX
02-JUN-2000 (first entry)

DE Streptococcus pneumoniae protein sequence ID.

XX
KW Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS;
bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism;
KW kidney disease; diabetes; immunosuppressive disorder; otitis media;
KW pneumococcal septicaemia; sinusitis; meningitis; therapy.

OS Streptococcus pneumoniae.

PN WO200006738-A2.

PD 10-FEB-2000.

PF 27-JUL-1999; 99WO-GB002452.

PR 27-JUL-1998; 98GB-00016336.

PR 19-MAR-1999; 99US-0125329P.

PA (MICR-) MICROBIAL TECHNIQS LTD.

PI Le Page RWF, Wells JM, Hanniffy SB, Hansbro PM;

XX WPI; 2000-195301/17.

DR N-PSDB; AA291805.

DR Streptococcal proteins and polynucleotides useful for diagnosis,

XX treatment and prophylaxis of bacterial infections.

PS Claim 2; Page 40; 76pp; English.

XX This sequence represents a Streptococcus pneumoniae protein of the
invention. The proteins (or their homologues, derivatives and/or
fragments) are useful as immunogens or antigens. Immunogenic or antigenic
compositions comprising the proteins are useful as vaccines and also in
diagnostic assays. The sequences are useful for the detection or
diagnosis of S. pneumoniae infection, by contacting a sample to be tested
with them. Agents capable of antagonising, inhibiting or interfering with
the function or expression of the protein or polypeptide are useful in
medical compositions in the treatment or prophylaxis of S. pneumoniae
infection. As the sequences can be used to treat S. pneumoniae infection,

CC they can be used to treat bacterial pneumonia, which has high rates in
CC young children, the elderly, and in patients with predisposing conditions
CC such as asplenia, heart, lung and kidney disease, diabetes, alcoholism,
CC or with immunosuppressive disorders, especially AIDS. They can also be
CC used to treat pneumococcal septicaemia, otitis media, sinusitis, and
CC meningitis
XX
SQ Sequence 279 AA;

Query Match 100.0%; Score 1387; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 5.8e-125;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGIALENVNTYQEGTGPLASALSDVSLTIEDGSYTALIGHTSGKSTILOLLNGLLVPS 60
Db 1 MGIALENVNTYQEGTGPLASALSDVSLTIEDGSYTALIGHTSGKSTILOLLNGLLVPS 60

Qy 61 QGSVRVFDTLITSTSKNDIRQIRKQVGLVFQFAENQIFETVLKDVAFQNFQVSEED 120
Db 61 QGSVRVFDTLITSTSKNDIRQIRKQVGLVFQFAENQIFETVLKDVAFQNFQVSEED 120

Qy 121 AVKTAREKALVGVIDESLFDSPPELGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
Db 121 AVKTAREKALVGVIDESLFDSPPELGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180

Qy 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVWME 240
Db 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVWME 240

Qy 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
Db 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279

RESULT 2
ABU02751
ID ABU02751 standard; protein; 279 AA.
XX
AC ABU02751;
XX
DT 23-OCT-2003 (revised)
DT 11-FEB-2003 (first entry)
XX
DE S. pneumoniae type 4 strain protein from coding region #2330.
XX
KW Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
KW antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
KW gene therapy; vaccine.
XX
OS Streptococcus pneumoniae; type 4 strain.
XX
PN WO200277021-A2.
XX
PD 03-OCT-2002.
PF 27-MAR-2002; 2002WO-IB002163.
XX
PR 27-MAR-2001; 2001GB-00007658.
XX
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
PI Massignani V, Tettelin H, Fraser C;
XX
DR WPI; 2003-040579/03.
DR N-PSDB; ABX08042.
XX
XX New proteins and nucleic acid molecules from Streptococcus pneumoniae,
PT useful as medicaments for treating or preventing a disease or infection
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
PT ear infection.
XX
PS Claim 1; SEQ ID NO 4660; 56pp; English.

XX
CC The invention relates to a protein comprising or having at least 50%
CC identity to any of the 2469 amino acid sequences, identified in the
CC specification (available on a computer readable format), or its fragment,
CC expressed from 2469 of 2489 identified DNA coding regions from the
CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
CC ABS56454. Also included are an antibody which binds one of the proteins,
CC treating a patient by administering the protein, DNA or antibody (in a
CC composition), a kit comprising first and second primers, which are the
CC nucleic acid cited above or fragments between nucleotides 8-100 of a
CC sequence not defined in the specification, for amplifying a target
CC the first primer is substantially complementary to the target sequence, where
CC and the second primer is substantially complementary to the complement of
CC the target sequence, and where the parts of the primers having
CC substantial complementarity define the termini of the target sequence to
CC be amplified, assay comprising contacting a test compound with the
CC protein, and determining whether the test compound binds to the protein
CC and a Streptococcus pneumoniae bacterium, where one or more genes
CC encoding the proteins has been rendered inactive. The proteins, nucleic
CC acid molecules, antibody and compositions are useful as medicaments for
CC treating or preventing a disease or infection due to streptococcus
CC bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis
CC media or ear infection. They are also useful in developing vaccines,
CC diagnostics and antibiotics. The methods are useful for identifying
CC immunodominant proteins. The present sequence is one of the 2469 proteins
CC expressed by the identified coding regions from the genomic sequence.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 279 AA;

Query Match 100.0%; Score 1387; DB 6; Length 279;
Best Local Similarity 100.0%; Pred. No. 5.8e-125;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGIALENVNTYQEGTGPLASALSDVSLTIEDGSYTALIGHTSGKSTILOLLNGLLVPS 60
Db 1 MGIALENVNTYQEGTGPLASALSDVSLTIEDGSYTALIGHTSGKSTILOLLNGLLVPS 60

Qy 61 QGSVRVFDTLITSTSKNDIRQIRKQVGLVFQFAENQIFETVLKDVAFQNFQVSEED 120
Db 61 QGSVRVFDTLITSTSKNDIRQIRKQVGLVFQFAENQIFETVLKDVAFQNFQVSEED 120

Qy 121 AVKTAREKALVGVIDESLFDSPPELGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
Db 121 AVKTAREKALVGVIDESLFDSPPELGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180

Qy 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVWME 240
Db 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVWME 240

Qy 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
Db 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279

RESULT 3
AA01016
ID AA01016 standard; protein; 279 AA.
XX
AC AA01016;
XX
DT 02-OCT-2001 (first entry)
XX
DE CFE 15 protein sequence.
XX
KW Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE;
KW CEG; Conserved Essential Gene; bacterial infection; antisense therapy;
KW antibiotic resistance.
XX


```
RESULT 5
ADR96203
ID ADR96203 standard; protein; 280 AA.
XX
AC ADR96203;
XX
DT 16-DEC-2004 (first entry)
XX
DE Novel S. pneumoniae protein sequence, SEQ ID 4838.
XX
KW Meningitis; bacteraemia; pneumonia; otitis media; vaccine;
KW bacterial infection.
XX
OS Streptococcus pneumoniae.
XX
PN US6800744-B1.
XX
PD 05-OCT-2004.
XX
PF 30-JUN-1998; 98US-00107433.
XX
PR 02-JUL-1997; 97US-0051553P.
XX
PR 12-MAY-1998; 98US-0085131P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI; 2004-697205/68.
XX
DR N-PSDB; ADR93600.
XX
PT New isolated nucleic acid encoding a Streptococcus pneumoniae
PT polypeptide, useful for diagnosing, preventing and/or treating
PT pathological conditions resulting from the bacterial infection.
XX
PS Disclosure; SEQ ID NO 4838; 151pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a sequence
CC encoding a Streptococcus pneumoniae ADR91366polypeptide, or its
CC fragments, with any of 9 fully defined sequences (appearing as ADR94308,
CC ADR94489, ADR94800, ADR94837, ADR94969, ADR95253, ADR95642, ADR95682,
CC ADR96079) or any of the fully defined sequences appearing as ADR91705,
CC ADR91886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or
CC ADR93476 or at least 20 or 30 consecutive nucleotides of the nucleotide
CC sequences, or at least 40, 60 or 300 consecutive nucleotides, which is
CC hybridizable under high stringency conditions to the nucleotide sequence.
CC The nucleic acids and proteins are chosen from 5206 disclosed sequences.
CC Also included are a recombinant expression vector comprising the isolated
CC nucleic acid cited above operably linked to a transcription regulatory
CC element, a cell comprising the recombinant expression vector and a probe
CC comprising at least 20 consecutive nucleotides of the nucleotide
CC sequences as cited above. The methods and compositions of the present
CC invention are useful for the diagnosis, prevention and/or treatment of
CC pathological conditions resulting from bacterial infection by
CC Streptococcus pneumoniae e.g. pneumonia, bacteraemia, meningitis and
CC otitis media. The present sequence is one of the 2603 disclosed S.
CC pneumoniae protein sequences. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=6800744B1.
XX
SQ Sequence 280 AA;
Query Match 99.9%; Score 1386; DB 8; Length 280;
Best Local Similarity 99.6%; Pred No. 7.3e-125;
Matches 278; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIALENVFTYQEGTPLASALSDVSLTIEDGYSYALIGHTGSGKSTIQLNGLVPS 60
DB 2 MGIALENVFTYQEGTPLASALSDVSLTIEDGYSYALIGHTGSGKSTIQLNGLVPS 61
QY 61 QGSVRVFTLITSTSKNDIRKQKGLVQFAENQIFETVLKDVAFGPNFGVSEED 120
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CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 279 AA;

Query Match 99.4%; Score 1378; DB 4; Length 279;
Best Local Similarity 99.3%; Pred. No. 4.3e-124;
Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIALENNVFTYQEGTFLASAAALSDVSLTIEDGSYTALIGHTGSGKSTILQLLNGLLVS 60
DB 1 MGIALENNVFIYQEGTFLASAAALSDVSLTIEDGSYTALIGHTGSGKSTILQLLNGLLVS 60
QY 61 QGSVRVFDLTITSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 QGSVRVFDLTITSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
QY 121 AVKTAREKALVGLIDESLDRSPFELSGGOMRVAIAGILAMEPAILVLDEPTAGLDPLG 180
DB 121 AVKTAREKALVGLIDESLDRSPFELSGGOMRVAIAGILAMEPAILVLDEPTAGLDPLG 180
QY 181 RKELMTLFLKKLHQSGMTIVLVTHLMDVAEYANQVYVMEKGRVLKGGKPSDVFQVVFME 240
DB 181 RKELMTLFLKKLHQSGMTIVLVTHLMDVAEYANQVYVMEKGRVLKGGKPSDVFQVVFME 240
QY 241 EVOLGVPKITAFCKRLADRGVSPKRLPIKIEEPKESLNG 279
DB 241 EVOLGVPKITAFCKRLADRGVSPKRLPIKIEEPKESLNG 279

RESULT 8
ABU44574
ID ABU44574 standard; protein; 280 AA.
XX
AC ABU44574;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #30101.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Streptococcus mutans.
XX
PN WO200277183-A2.
XX

CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 279 AA;

Query Match 99.4%; Score 1378; DB 4; Length 279;
Best Local Similarity 99.3%; Pred. No. 4.3e-124;
Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIALENNVFTYQEGTFLASAAALSDVSLTIEDGSYTALIGHTGSGKSTILQLLNGLLVS 60
DB 1 MGIALENNVFIYQEGTFLASAAALSDVSLTIEDGSYTALIGHTGSGKSTILQLLNGLLVS 60
QY 61 QGSVRVFDLTITSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 QGSVRVFDLTITSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
QY 121 AVKTAREKALVGLIDESLDRSPFELSGGOMRVAIAGILAMEPAILVLDEPTAGLDPLG 180
DB 121 AVKTAREKALVGLIDESLDRSPFELSGGOMRVAIAGILAMEPAILVLDEPTAGLDPLG 180
QY 181 RKELMTLFLKKLHQSGMTIVLVTHLMDVAEYANQVYVMEKGRVLKGGKPSDVFQVVFME 240
DB 181 RKELMTLFLKKLHQSGMTIVLVTHLMDVAEYANQVYVMEKGRVLKGGKPSDVFQVVFME 240
QY 241 EVOLGVPKITAFCKRLADRGVSPKRLPIKIEEPKESLNG 279
DB 241 EVOLGVPKITAFCKRLADRGVSPKRLPIKIEEPKESLNG 279

RESULT 7
ABU46314
ID ABU46314 standard; protein; 279 AA.
XX
AC ABU46314;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #31841.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Streptococcus pneumoniae.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
XX
PR 06-SEP-2001; 2001US-00948993.
XX
PR 25-OCT-2001; 2001US-0342923P.
XX
PR 08-FEB-2002; 2002US-00072851.
XX
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (BLIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlson KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA50184.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 74238; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression

Matches 191; Conservative 35; Mismatches 51; Indels 0; Gaps 0;	
QY	1 MGIALENNFTYQEGTPLASALSDVSLTIEDGSGYTAUGHTGSGKSTILQINGLLVPS 60
DB	1 MSINLQNSVYTYQAGTFEGRALFNILNDLGSYTAFTGHTGSGKSTIMQLLGLHVPT 60
QY	61 QGSVRVFDLTITSTKNDIROIKQVGLVFOFAENQIFETVLDKVAFGPQNGVSEED 120
DB	61 TGIVSVVDKQDITNHSKNKEIKIRKHVGLVFPFESQLFEETVLDKVAFGPQNGVSP 120
QY	121 AVKTAREKALVIGIDESLDFRSPFELSGGQMRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
DB	121 AEALAREKALVIGISENLFKNPFELSGGQMRVAIAGILAMQPKVLVLDDEPTAGLDPKG 180
QY	181 RKELMTLFPKLLHQSGMTIVLVTHLMDDDVAEYANQVVMKGLVKGKSDVQDVVEME 240
DB	181 RKELMTIFPKLLHQSGMTIVLVTHLMDDDVANYADFYVLDKGIILSGKPKTIQQVSLLE 240
QY	241 EVQLGVPKITAFCRLADRGVSFKRLPIKIEEPKESL 277
DB	241 KKQLGVPKVKLAQRLVDRGIPISLLPITLEELREVL 277
RESULT 10	
ABU46897	
ID	ABU46897 standard; protein; 280 AA.
XX	
AC	ABU46897;
DT	
DT	19-JUN-2003 (first entry)
XX	
DE	Protein encoded by Prokaryotic essential gene #32424.
XX	
KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX	
OS	Streptococcus pyogenes.
XX	
PN	WO200277183-A2.
XX	
PD	03-OCT-2002.
XX	
PF	21-MAR-2002; 2002WO-US009107.
XX	
PR	21-MAR-2001; 2001US-00815242.
PR	06-SEP-2001; 2001US-00948993.
PR	25-OCT-2001; 2001US-0342923P.
PR	08-FEB-2002; 2002US-00072851.
PR	06-MAR-2002; 2002US-0362699P.
XX	
PA	(BLIT-) ELITRA PHARM INC.
XX	
PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX	
DR	WPI; 2003-029926/02.
DR	N-PSDB; ACA50767.
XX	
XX	New antisense nucleic acids, useful for identifying proteins or screening
PT	for homologous nucleic acids required for cellular proliferation to
PT	isolate candidate molecules for rational drug discovery programs.
XX	
PS	Claim 25; SEQ ID NO 74821; 1766pp; English.
XX	
CC	The invention relates to an isolated nucleic acid comprising any one of
CC	the 6213 antisense sequences given in the specification where expression
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:
CC	(1) a vector comprising a promoter operably linked to the nucleic acid
CC	encoding a polypeptide whose expression is inhibited by the antisense
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC	polypeptide or its fragment whose expression is inhibited by the
CC	antisense nucleic acid; (4) an antibody capable of specifically binding
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC	proliferation or the activity of a gene in an operon required for

Query Match 70.0%; Score 971; DB 6; Length 280;	
Best Local Similarity 69.0%; Pred. No. 7e-85;	
Matches 191; Conservative 35; Mismatches 51; Indels 0; Gaps 0;	
QY	1 MGIALENNFTYQEGTPLASALSDVSLTIEDGSGYTAUGHTGSGKSTILQINGLLVPS 60
DB	1 MSINLQNSVYTYQAGTFEGRALFNILNDLGSYTAFTGHTGSGKSTIMQLLGLHVPT 60
QY	61 QGSVRVFDLTITSTKNDIROIKQVGLVFOFAENQIFETVLDKVAFGPQNGVSEED 120
DB	61 TGIVSVVDKQDITNHSKNKEIKIRKHVGLVFPFESQLFEETVLDKVAFGPQNGVSP 120
QY	121 AVKTAREKALVIGIDESLDFRSPFELSGGQMRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
DB	121 AEALAREKALVIGISENLFKNPFELSGGQMRVAIAGILAMQPKVLVLDDEPTAGLDPKG 180
QY	181 RKELMTLFPKLLHQSGMTIVLVTHLMDDDVAEYANQVVMKGLVKGKSDVQDVVEME 240
DB	181 RKELMTIFPKLLHQSGMTIVLVTHLMDDDVANYADFYVLDKGIILSGKPKTIQQVSLLE 240
QY	241 EVQLGVPKITAFCRLADRGVSFKRLPIKIEEPKESL 277
DB	241 KKQLGVPKVKLAQRLVDRGIPISLLPITLEELREVL 277
RESULT 11	
ABP26997	
ID	ABP26997 standard; protein; 280 AA.
XX	
AC	ABP26997;
DT	
DT	02-JUL-2002 (first entry)
XX	
DE	Streptococcus polypeptide SEQ ID NO 3170.
XX	
KW	Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW	group A streptococcus; Streptococcus pyogenes; antibacterial;
KW	antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX	
OS	Streptococcus agalactiae.
XX	
PN	WO200234771-A2.
XX	
PD	02-MAY-2002.
XX	
PF	29-OCT-2001; 2001WO-GB004789.
XX	
PR	27-OCT-2000; 2000GB-00026333.
PR	24-NOV-2000; 2000GB-00028727.

PR 07-MAR-2001; 2001GB-00005640.
XX (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX Telford J, Massignani V, Margarit Y Rosi, Grandi G, Fraser C;
PI Tettelin H;
XX WPI; 2002-352536/38.
DR N-PSDB; ABN67628.
XX New Streptococcus protein for the treatment or prevention of infection or
XX disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.
XX Claim 1; Page 3470; 4525pp; English.
PS
XX The invention relates to a protein (ABP25413-ABP30895) from group B
XX streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and anti-inflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
XX Streptococcus proteins
XX
SQ Sequence 280 AA;
Query Match 68.3%; Score 948; DB 5; Length 280;
Best Local Similarity 66.8%; Pred. No. 1.2e-82;
Matches 185; Conservative 39; Mismatches 53; Indels 0; Gaps 0;
QY 1 MGIALENVFTYQEGTTPPLASALSDVSLTIEDGSYTALIGHTGSKSTILQLLNGLLVP 60
DB 1 MGIEPKNVSYTYQAGTPEGRALFDVNLKIEDASYTAFIGHTGSKSTIMQLLGLHIPT 60
QY 61 QGSVRFDTLITSTSKNDIRQKQGLVGFQFAENQIFETVLKDVAFGPNQFVSEED 120
DB 61 KGEVIVDDFSIKAGDKNKEIKFIRKQGLVGFQFPESQLFEETVLKDVAFGPNQFVSEED 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAILLVDEPTAGLDPLG 180
DB 121 AERLAEEKLRLVIGISEDLFDKNPFELSGQMRRAIAGILAMEPAILLVDEPTAGLDPLG 180
QY 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVAVYANQVYVMEKGRVKGKPSDVDFQVPM 240
DB 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVAVYANQVYVMEKGRVKGKPSDVDFQVPM 240
QY 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
DB 241 SKQLGVPKITKPAQLSHKGLNPLSLPITINEFVEAI 277
RESULT 12
ADK99875
ID ADK99875 standard; protein; 280 AA.
XX ADK99875;
AC ADK99875;
XX 20-MAY-2004 (first entry)
DT Streptococcus agalactiae ORF SAG2150-related protein 1.
DE Streptococcus agalactiae ORF SAG2150-related protein 1.
XX immunogenic composition; group B Streptococcus; GBS; antibacterial;

streptococcal infection; vaccine; SAG.
XX Streptococcus agalactiae 2603V/R.
XX WO2004018646-A2.
XX 04-MAR-2004.
XX 26-AUG-2003; 2003WO-US026827.
XX 26-AUG-2002; 2002US-0406237P.
PR 27-AUG-2002; 2002US-0406676P.
PR 28-AUG-2002; 2002US-0406757P.
XX (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX Tettelin H, Massignani V;
XX WPI; 2004-248071/23.
XX Immunogenic composition useful as a vaccine for treating or preventing
PT streptococcal infections, comprises group B Streptococcus polypeptides.
XX Claim 10; SEQ ID NO 7912; 1194pp; English.
PS The invention relates to a novel immunogenic composition comprising a
XX combination of 2-5 group B Streptococcus (GBS) polypeptides. Each
CC polypeptide is encoded by a GBS polynucleotide sequence which is
CC homologous to a polynucleotide sequence of group A Streptococcus (GAS),
CC Streptococcus pneumoniae and/or at least one other GBS serotype. The
CC composition of the invention demonstrates antibacterial activity whilst
CC the polypeptides and polynucleotides may be useful in assays to diagnose
CC and identify streptococcal infections or for identifying, screening and
CC developing vaccines and other treatments for streptococcal infections.
CC The current sequence is that of a Streptococcus agalactiae ORF SAG
XX protein of the invention.
XX
SQ Sequence 280 AA;
Query Match 68.3%; Score 948; DB 8; Length 280;
Best Local Similarity 66.8%; Pred. No. 1.2e-82;
Matches 185; Conservative 39; Mismatches 53; Indels 0; Gaps 0;
QY 1 MGIALENVFTYQEGTTPPLASALSDVSLTIEDGSYTALIGHTGSKSTILQLLNGLLVP 60
DB 1 MGIEPKNVSYTYQAGTPEGRALFDVNLKIEDASYTAFIGHTGSKSTIMQLLGLHIPT 60
QY 61 QGSVRFDTLITSTSKNDIRQKQGLVGFQFAENQIFETVLKDVAFGPNQFVSEED 120
DB 61 KGEVIVDDFSIKAGDKNKEIKFIRKQGLVGFQFPESQLFEETVLKDVAFGPNQFVSEED 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAILLVDEPTAGLDPLG 180
DB 121 AERLAEEKLRLVIGISEDLFDKNPFELSGQMRRAIAGILAMEPAILLVDEPTAGLDPLG 180
QY 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVAVYANQVYVMEKGRVKGKPSDVDFQVPM 240
DB 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVAVYANQVYVMEKGRVKGKPSDVDFQVPM 240
QY 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
DB 241 SKQLGVPKITKPAQLSHKGLNPLSLPITINEFVEAI 277
RESULT 13
ADK99877
ID ADK99877 standard; protein; 279 AA.
XX ADK99877;
AC ADK99877;
XX 20-MAY-2004 (first entry)
DT Streptococcus agalactiae ORF SAG2150-related protein 1.
DE Streptococcus agalactiae ORF SAG2150-related protein 1.
XX immunogenic composition; group B Streptococcus; GBS; antibacterial;

Streptococcus agalactiae ORF SAG2150-related protein 3.
immunogenic composition; group B Streptococcus; GBS; antibacterial;
streptococcal infection; vaccine; SAG.
Streptococcus agalactiae.
WO2004018646-A2.
04-MAR-2004.
26-AUG-2003; 2003WO-US026827.
26-AUG-2002; 2002US-0406237P.
27-AUG-2002; 2002US-040676P.
28-AUG-2002; 2002US-0406757P.
(CHIR) CHIRON CORP.
(GENO-) INST GENOMIC RES.
Tettelin H, Masignani V;
WPI; 2004-248071/23.
Immunogenic composition useful as a vaccine for treating or preventing
streptococcal infections, comprises group B Streptococcus polypeptides.
Claim 10; SEQ ID NO 7914; 1194pp; English.
The invention relates to a novel immunogenic composition comprising a
combination of 2-5 group B Streptococcus (GBS) polypeptides. Each
polypeptide is encoded by a GBS polynucleotide sequence which is
homologous to a polynucleotide sequence of group A Streptococcus (GAS),
Streptococcus pneumoniae and/or at least one other GBS serotype. The
composition of the invention demonstrates antibacterial activity whilst
the polypeptides and polynucleotides may be useful in assays to diagnose
and identify streptococcal infections or for identifying, screening and
developing vaccines and other treatments for streptococcal infections.
The current sequence is that of a Streptococcus agalactiae ORF SAG
protein of the invention.
SQ Sequence 279 AA;
Query Match 68.0%; Score 943; DB 8; Length 279;
Best Local Similarity 66.7%; Pred. No. 3.5e-82;
Matches 184; Conservative 39; Mismatches 53; Indels 0; Gaps 0;
QY 2 GIALNNVFTYQSGTPLASAAALSDVSLTIEDGYSYALIGHTSGKSTILQLLGLLVPSQ 61
Db 1 GIEFNVSYYTQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGKSTIMQLGLHIPTK 60
QY 62 GSVRVFDTLITSTSKNDIRQIRKQVGLVFPQAEQIFETVLKDVAFQPNFGVSEDA 121
Db 61 GEIVVDVDFSLKAGDKNKEIKFIRKQVGLVFPQAEQIFETVLKDVAFQPNFGISQIEA 120
QY 122 VKTAREKALVIGIDESLFRSPPELSCGQRRVAIAGILAMEPAAILVLDPTAGLDPLGR 181
Db 121 ERLAEKRLVIGISELFDKNPELSCGQRRVAIAGILAMEPKVLVLDPTAGLDPKGR 180
QY 182 KELMTLPKLLHOSGMTIVLVTHLMDVDAEVANOVYVMEKRLVKGKPSDVFDVVFME 241
Db 181 KELMTLPKLLHOSGMTIVLVTHLMDVDAEVANOVYVMEKRLVKGKPSDVFDVVFME 240
QY 242 VOLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
Db 241 KQLGVPKITKFAQLRSHKGLNPLSLPITINEFVEAI 276
RESULT 14
ADK99878
ID ADK99878 standard; protein; 279 AA.
XX AC ADK99878;

20-MAY-2004 (first entry)
Streptococcus agalactiae ORF SAG2150-related protein 4.
immunogenic composition; group B Streptococcus; GBS; antibacterial;
streptococcal infection; vaccine; SAG.
Streptococcus agalactiae.
WO2004018646-A2.
04-MAR-2004.
26-AUG-2003; 2003WO-US026827.
26-AUG-2002; 2002US-0406237P.
27-AUG-2002; 2002US-040676P.
28-AUG-2002; 2002US-0406757P.
(CHIR) CHIRON CORP.
(GENO-) INST GENOMIC RES.
Tettelin H, Masignani V;
WPI; 2004-248071/23.
Immunogenic composition useful as a vaccine for treating or preventing
streptococcal infections, comprises group B Streptococcus polypeptides.
Claim 10; SEQ ID NO 7915; 1194pp; English.
The invention relates to a novel immunogenic composition comprising a
combination of 2-5 group B Streptococcus (GBS) polypeptides. Each
polypeptide is encoded by a GBS polynucleotide sequence which is
homologous to a polynucleotide sequence of group A Streptococcus (GAS),
Streptococcus pneumoniae and/or at least one other GBS serotype. The
composition of the invention demonstrates antibacterial activity whilst
the polypeptides and polynucleotides may be useful in assays to diagnose
and identify streptococcal infections or for identifying, screening and
developing vaccines and other treatments for streptococcal infections.
The current sequence is that of a Streptococcus agalactiae ORF SAG
protein of the invention.
SQ Sequence 279 AA;
Query Match 68.0%; Score 943; DB 8; Length 279;
Best Local Similarity 66.7%; Pred. No. 3.5e-82;
Matches 184; Conservative 39; Mismatches 53; Indels 0; Gaps 0;
QY 2 GIALNNVFTYQSGTPLASAAALSDVSLTIEDGYSYALIGHTSGKSTILQLLGLLVPSQ 61
Db 1 GIEFNVSYYTQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGKSTIMQLGLHIPTK 60
QY 62 GSVRVFDTLITSTSKNDIRQIRKQVGLVFPQAEQIFETVLKDVAFQPNFGVSEDA 121
Db 61 GEIVVDVDFSLKAGDKNKEIKFIRKQVGLVFPQAEQIFETVLKDVAFQPNFGISQIEA 120
QY 122 VKTAREKALVIGIDESLFRSPPELSCGQRRVAIAGILAMEPAAILVLDPTAGLDPLGR 181
Db 121 ERLAEKRLVIGISELFDKNPELSCGQRRVAIAGILAMEPKVLVLDPTAGLDPKGR 180
QY 182 KELMTLPKLLHOSGMTIVLVTHLMDVDAEVANOVYVMEKRLVKGKPSDVFDVVFME 241
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QY 242 VOLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
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RESULT 15
ADK99876

Search completed: October 28, 2005, 17:50:02
Job time : 175 secs

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ID ADK99876 standard; protein; 279 AA.
XX AC ADK99876;
XX DT 20-MAY-2004 (first entry)
XX DE Streptococcus agalactiae ORF SAG2150-related protein 2.
XX KW immunogenic composition; group B Streptococcus; GBS; antibacterial;
XX KW streptococcal infection; vaccine; SAG.
XX OS Streptococcus agalactiae.
XX PN WO2004018646-A2.
XX PD 04-MAR-2004.
XX PF 26-AUG-2003; 2003WO-US026827.
XX PR 26-AUG-2002; 2002US-0406237P.
XX PR 27-AUG-2002; 2002US-0406676P.
XX PR 28-AUG-2002; 2002US-0406757P.
XX PA (CHIR ) CHIRON CORP.
XX PA (GENO-) INST GENOMIC RES.
XX PI Tettelin H, Massignani V;
XX DR WPI; 2004-248071/23.
XX PT Immunogenic composition useful as a vaccine for treating or preventing
XX PT streptococcal infections, comprises group B Streptococcus polypeptides.
XX PS Claim 10; SEQ ID NO 7913; 1194pp; English.
XX CC The invention relates to a novel immunogenic composition comprising a
XX CC combination of 2-5 group B Streptococcus (GBS) polypeptides. Each
XX CC polypeptide is encoded by a GBS polynucleotide sequence which is
XX CC homologous to a polynucleotide sequence of group A Streptococcus (GAS),
XX CC Streptococcus pneumoniae and/or at least one other GBS serotype. The
XX CC composition of the invention demonstrates antibacterial activity whilst
XX CC the polypeptides and polynucleotides may be useful in assays to diagnose
XX CC and identify streptococcal infections or for identifying, screening and
XX CC developing vaccines and other treatments for streptococcal infections.
XX CC The current sequence is that of a Streptococcus agalactiae ORF SAG
XX CC protein of the invention.
SQ Sequence 279 AA;

Query Match 68.0%; Score 943; DB 8; Length 279;
Best Local Similarity 66.7%; Pred. No. 3.5e-82;
Matches 184; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: October 28, 2005, 18:04:45 ; Search time 43 Seconds
(without alignments)
484.351 Million cell updates/sec

Title: US-09-769-744D-26

Perfect score: 279

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	11	3.9	300	4	US-09-861-451A-42
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9	10	3.6	288	3	US-09-134-001C-3292
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11	10	3.6	619	4	US-09-252-991A-21585
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103	7	2.5	272	1	US-08-709-177-84	Sequence 84, Appl	176	7	2.5	310	4	US-09-614-912-202	Sequence 202, Appl
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113	7	2.5	278	4	US-08-635-886C-265	Sequence 265, Ap	186	7	2.5	315	4	US-09-107-433-3914	Sequence 3914, Ap
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115	7	2.5	278	4	US-08-635-886C-267	Sequence 267, Ap	188	7	2.5	316	4	US-09-538-092-69	Sequence 69, Appl
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124	7	2.5	278	4	US-08-635-886C-276	Sequence 276, Ap	197	7	2.5	338	4	US-09-614-912-150	Sequence 150, Ap
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152	7	2.5	295	3	US-08-892-704-2	Sequence 2, Appl	225	7	2.5	375	4	US-09-328-352-5422	Sequence 5422, Ap
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156	7	2.5	299	1	US-08-709-173-68	Sequence 68, Appl	229	7	2.5	424	4	US-09-107-433-3815	Sequence 3815, Ap
157	7	2.5	299	2	US-08-709-177-68	Sequence 68, Appl	230	7	2.5	429	4	US-09-902-540-10768	Sequence 10768, A
158	7	2.5	299	2	US-08-709-177-68	Sequence 68, Appl	231	7	2.5	433	4	US-09-902-540-12518	Sequence 12518, A
159	7	2.5	300	4	US-09-134-000C-3733	Sequence 3733, Ap	232	7	2.5	444	4	US-09-902-540-16479	Sequence 16479, A
160	7	2.5	300	4	US-09-355-040-1	Sequence 1, Appl	233	7	2.5	461	4	US-08-833-678A-2	Sequence 2, Appl
161	7	2.5	301	3	US-08-829-525-24	Sequence 24, Appl	234	7	2.5	465	3	US-08-529-169A-2	Sequence 2, Appl
162	7	2.5	301	3	US-08-609-583A-24	Sequence 24, Appl	235	7	2.5	465	4	US-09-483-799-2	Sequence 2, Appl
163	7	2.5	301	3	US-08-937-399-24	Sequence 24, Appl	236	7	2.5	465	4	US-09-248-796A-22442	Sequence 22442, A
164	7	2.5	301	4	US-09-310-367-24	Sequence 24, Appl	237	7	2.5	475	4	US-09-252-991A-27210	Sequence 27210, A
165	7	2.5	301	4	US-09-032-337-24	Sequence 24, Appl	238	7	2.5	490	4	US-09-902-540-11335	Sequence 11335, A
166	7	2.5	302	3	US-09-464-231-24	Sequence 24, Appl	239	7	2.5	500	4	US-10-029-180-6	Sequence 6, Appl
167	7	2.5	302	3	US-08-511-759B-9	Sequence 9, Appl	240	7	2.5	504	4	US-09-489-039A-1262	Sequence 1262, A
168	7	2.5	302	3	US-09-592-197-9	Sequence 9, Appl	241	7	2.5	505	3	US-08-867-611-59	Sequence 59, Appl
169	7	2.5	302	3	US-08-892-704-9	Sequence 9, Appl	242	7	2.5	513	4	US-09-690-359-59	Sequence 59, Appl
170	7	2.5	302	4	US-09-438-185A-203	Sequence 203, Ap	243	7	2.5	513	4	US-09-583-110-2771	Sequence 2771, Ap
171	7	2.5	307	4	US-09-197-970B-3	Sequence 3, Appl	244	7	2.5	521	4	US-09-603-208A-150	Sequence 150, Ap
172	7	2.5	308	4	US-09-711-164-392	Sequence 392, Ap	245	7	2.5	521	4	US-09-446-301A-49	Sequence 49, Appl
173	7	2.5	309	1	US-08-463-092B-8	Sequence 8, Appl	246	7	2.5	522	4		

247	7	2.5	522	4	US-09-099-932-49	Sequence 49, Appl	320	7	2.5	686	1	US-08-709-173-70	Sequence 70, Appl
248	7	2.5	532	4	US-09-902-540-15585	Sequence 15585, A	321	7	2.5	686	2	US-08-709-177-70	Sequence 70, Appl
249	7	2.5	540	4	US-09-902-540-16745	Sequence 16745, A	322	7	2.5	686	4	US-09-881-239-3	Sequence 3, Appl
250	7	2.5	546	4	US-09-107-532A-3981	Sequence 3981, Ap	323	7	2.5	686	4	US-09-881-654-2	Sequence 2, Appl
251	7	2.5	547	4	US-09-603-208A-290	Sequence 290, App	324	7	2.5	686	4	US-10-637-323-2	Sequence 2, Appl
252	7	2.5	548	4	US-09-107-532A-6627	Sequence 6627, Ap	325	7	2.5	687	1	US-08-188-281B-14	Sequence 14, Appl
253	7	2.5	554	4	US-09-614-912-200	Sequence 200, App	326	7	2.5	687	5	PCT-US94-07280-14	Sequence 14, Appl
254	7	2.5	554	4	US-09-902-540-16735	Sequence 16735, A	327	7	2.5	687	5	PCT-US95-01087-14	Sequence 14, Appl
255	7	2.5	569	4	US-09-134-000C-5386	Sequence 5386, Ap	328	7	2.5	694	2	US-08-895-522-3	Sequence 3, Appl
256	7	2.5	575	4	US-09-134-000C-5386	Sequence 5386, Ap	329	7	2.5	694	3	US-09-195-391-3	Sequence 3, Appl
257	7	2.5	580	3	US-09-134-001C-5611	Sequence 5611, Ap	330	7	2.5	715	4	US-09-543-681A-4943	Sequence 4943, Ap
258	7	2.5	582	4	US-09-489-039A-12080	Sequence 12080, A	331	7	2.5	715	4	US-09-881-239-1	Sequence 1, Appl
259	7	2.5	590	3	US-08-850-328-3	Sequence 3, Appl	332	7	2.5	728	4	US-08-444-818-148	Sequence 148, App
260	7	2.5	593	4	US-09-543-681A-5368	Sequence 5368, Ap	333	7	2.5	739	3	US-08-895-522-1	Sequence 1, Appl
261	7	2.5	594	4	US-09-107-532A-7250	Sequence 7250, Ap	334	7	2.5	747	3	US-09-195-391-1	Sequence 1, Appl
262	7	2.5	609	1	US-08-324-977-40	Sequence 40, Appl	335	7	2.5	747	3	US-09-603-208A-146	Sequence 146, App
263	7	2.5	609	2	US-08-384-616-40	Sequence 40, Appl	336	7	2.5	780	4	US-08-867-611-4	Sequence 4, Appl
264	7	2.5	609	3	US-08-904-686A-40	Sequence 40, Appl	337	7	2.5	781	4	US-09-690-359-4	Sequence 4, Appl
265	7	2.5	609	3	US-09-315-850-40	Sequence 40, Appl	338	7	2.5	781	4	US-09-690-359-4	Sequence 4, Appl
266	7	2.5	613	4	US-10-104-966-6	Sequence 6, Appl	339	7	2.5	781	5	PCT-US92-06965A-9	Sequence 9, Appl
267	7	2.5	623	4	US-09-252-991A-31173	Sequence 31173, A	340	7	2.5	798	1	US-08-190-802A-64	Sequence 64, Appl
268	7	2.5	628	4	US-09-360-545-4	Sequence 4, Appl	341	7	2.5	798	1	US-08-802A-68	Sequence 2, Appl
269	7	2.5	628	4	US-09-398-395A-20	Sequence 20, Appl	342	7	2.5	798	2	US-08-308-818-2	Sequence 2, Appl
270	7	2.5	628	4	US-09-887-586A-20	Sequence 20, Appl	343	7	2.5	798	3	US-08-477-346-64	Sequence 64, Appl
271	7	2.5	628	4	US-09-895-752-20	Sequence 20, Appl	344	7	2.5	798	3	US-08-477-346-64	Sequence 64, Appl
272	7	2.5	628	4	US-09-903-012B-20	Sequence 20, Appl	345	7	2.5	798	3	US-08-473-089-64	Sequence 64, Appl
273	7	2.5	631	1	US-08-700-356-1	Sequence 1, Appl	346	7	2.5	798	3	US-08-473-089-64	Sequence 64, Appl
274	7	2.5	631	2	US-08-936-865-1	Sequence 1, Appl	347	7	2.5	798	4	US-08-487-072A-64	Sequence 64, Appl
275	7	2.5	631	2	US-08-833-678A-1	Sequence 1, Appl	348	7	2.5	829	4	US-08-487-072A-68	Sequence 68, Appl
276	7	2.5	631	3	US-09-128-314-2	Sequence 2, Appl	349	7	2.5	829	4	US-08-444-818-69	Sequence 69, Appl
277	7	2.5	631	3	US-08-529-169A-1	Sequence 1, Appl	350	7	2.5	841	1	US-08-350-884-86	Sequence 86, Appl
278	7	2.5	631	3	US-09-483-799-1	Sequence 1, Appl	351	7	2.5	841	1	US-08-709-173-86	Sequence 86, Appl
279	7	2.5	632	3	US-09-198-723A-23	Sequence 23, Appl	352	7	2.5	841	2	US-08-709-177-86	Sequence 86, Appl
280	7	2.5	632	4	US-09-684-881-23	Sequence 23, Appl	353	7	2.5	911	3	US-08-667-611-52	Sequence 52, Appl
281	7	2.5	633	4	US-09-583-110-3803	Sequence 3803, Ap	354	7	2.5	911	3	US-09-690-359-53	Sequence 53, Appl
282	7	2.5	633	3	US-09-288-391-25	Sequence 25, Appl	355	7	2.5	973	3	US-08-867-611-53	Sequence 53, Appl
283	7	2.5	646	3	US-09-198-723A-60	Sequence 60, Appl	356	7	2.5	973	3	US-09-690-359-53	Sequence 53, Appl
284	7	2.5	646	3	US-09-198-723A-63	Sequence 63, Appl	357	7	2.5	981	4	US-09-252-991A-18616	Sequence 18616, A
285	7	2.5	646	3	US-09-198-723A-66	Sequence 66, Appl	358	7	2.5	981	4	US-08-867-611-54	Sequence 54, Appl
286	7	2.5	646	3	US-09-198-723A-69	Sequence 69, Appl	359	7	2.5	981	4	US-09-690-359-54	Sequence 54, Appl
287	7	2.5	646	3	US-09-198-723A-72	Sequence 72, Appl	360	7	2.5	992	4	US-09-690-359-54	Sequence 54, Appl
288	7	2.5	646	4	US-09-684-881-60	Sequence 60, Appl	361	7	2.5	1021	1	US-07-910-760-12	Sequence 12, Appl
289	7	2.5	646	4	US-09-684-881-63	Sequence 63, Appl	362	7	2.5	1021	1	US-08-440-519-12	Sequence 12, Appl
290	7	2.5	646	4	US-09-684-881-66	Sequence 66, Appl	363	7	2.5	1021	3	US-08-440-549-12	Sequence 12, Appl
291	7	2.5	646	4	US-09-684-881-69	Sequence 69, Appl	364	7	2.5	1099	4	US-09-881-654-4	Sequence 4, Appl
292	7	2.5	646	4	US-09-684-881-72	Sequence 72, Appl	365	7	2.5	1099	4	US-09-881-654-4	Sequence 4, Appl
293	7	2.5	650	4	US-09-107-433-3849	Sequence 3849, Ap	366	7	2.5	1147	1	US-10-637-323-4	Sequence 38, Appl
294	7	2.5	660	4	US-09-583-110-4478	Sequence 4478, Ap	367	7	2.5	1147	2	US-08-131-365B-38	Sequence 38, Appl
295	7	2.5	664	4	US-09-107-433-3490	Sequence 3490, Ap	368	7	2.5	1164	4	US-08-668-123-38	Sequence 38, Appl
296	7	2.5	665	4	US-09-543-376B-1	Sequence 1, Appl	369	7	2.5	1196	4	US-09-949-016-9845	Sequence 9845, Ap
297	7	2.5	665	4	US-09-543-376B-2	Sequence 2, Appl	370	7	2.5	1272	4	US-09-949-016-7472	Sequence 7472, Ap
298	7	2.5	665	4	US-09-543-376B-3	Sequence 3, Appl	371	7	2.5	1307	1	US-08-395-246C-2	Sequence 2, Appl
299	7	2.5	666	3	US-09-198-723A-11	Sequence 11, Appl	372	7	2.5	1308	2	US-08-936-644-2	Sequence 2, Appl
300	7	2.5	666	3	US-09-198-723A-12	Sequence 12, Appl	373	7	2.5	1308	3	US-09-352-552-2	Sequence 2, Appl
301	7	2.5	666	3	US-09-198-723A-13	Sequence 13, Appl	374	7	2.5	1375	3	US-08-665-259-26	Sequence 26, Appl
302	7	2.5	666	3	US-09-198-723A-14	Sequence 14, Appl	375	7	2.5	1375	3	US-08-762-500-26	Sequence 26, Appl
303	7	2.5	666	3	US-09-198-723A-15	Sequence 15, Appl	376	7	2.5	1422	4	US-08-469-260A-83	Sequence 83, Appl
304	7	2.5	666	3	US-09-198-723A-16	Sequence 16, Appl	377	7	2.5	1422	4	US-08-488-446-83	Sequence 83, Appl
305	7	2.5	666	3	US-09-198-723A-17	Sequence 17, Appl	378	7	2.5	1422	4	US-08-467-344A-83	Sequence 83, Appl
306	7	2.5	666	3	US-09-198-723A-18	Sequence 18, Appl	379	7	2.5	1457	3	US-08-444-550B-83	Sequence 83, Appl
307	7	2.5	666	3	US-09-684-881-11	Sequence 11, Appl	380	7	2.5	1457	3	US-08-665-259-27	Sequence 27, Appl
308	7	2.5	666	4	US-09-684-881-12	Sequence 12, Appl	381	7	2.5	1472	4	US-08-762-500-27	Sequence 27, Appl
309	7	2.5	666	4	US-09-684-881-13	Sequence 13, Appl	382	7	2.5	1472	4	US-09-032-438C-119	Sequence 119, App
310	7	2.5	666	4	US-09-684-881-14	Sequence 14, Appl	383	7	2.5	1475	2	US-09-256-703-2	Sequence 2, Appl
311	7	2.5	666	4	US-09-684-881-15	Sequence 15, Appl	384	7	2.5	1479	3	US-08-951-912-4	Sequence 4, Appl
312	7	2.5	666	4	US-09-684-881-16	Sequence 16, Appl	385	7	2.5	1479	3	US-09-174-077-1	Sequence 2, Appl
313	7	2.5	666	4	US-09-684-881-17	Sequence 17, Appl	386	7	2.5	1480	1	US-07-637-621-2	Sequence 2, Appl
314	7	2.5	666	4	US-09-684-881-18	Sequence 18, Appl	387	7	2.5	1480	1	US-08-136-742A-2	Sequence 2, Appl
315	7	2.5	672	3	US-09-198-723A-19	Sequence 19, Appl	388	7	2.5	1480	1	US-08-135-809A-2	Sequence 2, Appl
316	7	2.5	672	3	US-09-198-723A-20	Sequence 20, Appl	389	7	2.5	1480	1	US-08-466-886-17	Sequence 17, Appl
317	7	2.5	672	4	US-09-684-881-19	Sequence 19, Appl	390	7	2.5	1480	2	US-08-951-912-2	Sequence 2, Appl
318	7	2.5	672	4	US-09-684-881-20	Sequence 20, Appl	391	7	2.5	1480	2	US-08-951-912-6	Sequence 6, Appl
319	7	2.5	686	1	US-08-350-884-70	Sequence 70, Appl	392	7	2.5	1480	2	US-08-469-461-2	Sequence 2, Appl

393	7	2.5	1480	2	US-08-591-605-2	Sequence 2, Appli	466	7	2.5	2307	4	US-10-191-966-16	Sequence 16, Appli
394	7	2.5	1480	2	US-08-455-552A-14	Sequence 14, Appli	467	7	2.5	2336	3	US-08-444-818-75	Sequence 75, Appli
395	7	2.5	1480	3	US-07-890-609-2	Sequence 2, Appli	468	7	2.5	2560	4	US-09-949-016-11554	Sequence 11554, A
396	7	2.5	1480	3	US-07-890-609-4	Sequence 4, Appli	469	7	2.5	2620	1	US-08-324-977-32	Sequence 32, Appli
397	7	2.5	1480	3	US-09-248-026-2	Sequence 2, Appli	470	7	2.5	2620	2	US-08-384-616-32	Sequence 32, Appli
398	7	2.5	1480	3	US-08-469-617-17	Sequence 17, Appli	471	7	2.5	2620	2	US-08-904-686A-32	Sequence 32, Appli
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400	7	2.5	1480	3	US-08-681-838A-3	Sequence 3, Appli	473	7	2.5	2621	1	US-08-324-977-36	Sequence 36, Appli
401	7	2.5	1480	3	US-09-174-077-2	Sequence 2, Appli	474	7	2.5	2621	2	US-08-384-616-36	Sequence 36, Appli
402	7	2.5	1480	3	US-09-174-077-6	Sequence 6, Appli	475	7	2.5	2621	2	US-08-904-686A-36	Sequence 36, Appli
403	7	2.5	1480	3	US-09-425-453A-2	Sequence 2, Appli	476	7	2.5	2621	3	US-09-315-850-36	Sequence 36, Appli
404	7	2.5	1480	4	US-09-425-453A-4	Sequence 4, Appli	477	7	2.5	2621	3	US-08-444-818-89	Sequence 89, Appli
405	7	2.5	1480	4	US-09-425-453A-6	Sequence 6, Appli	478	7	2.5	2621	3	US-08-469-260A-394	Sequence 394, Appli
406	7	2.5	1480	4	US-09-425-453A-8	Sequence 8, Appli	479	7	2.5	2621	4	US-08-488-446-394	Sequence 394, App
407	7	2.5	1480	4	US-09-425-453A-10	Sequence 10, Appli	480	7	2.5	2621	4	US-08-467-344A-394	Sequence 394, App
408	7	2.5	1480	4	US-09-425-453A-12	Sequence 12, Appli	481	7	2.5	2621	4	US-08-424-550B-394	Sequence 394, App
409	7	2.5	1480	4	US-09-425-453A-14	Sequence 14, Appli	482	7	2.5	2621	2	US-08-466-975A-23	Sequence 23, Appli
410	7	2.5	1480	4	US-09-425-453A-16	Sequence 16, Appli	483	7	2.5	2621	2	US-08-391-671A-23	Sequence 23, Appli
411	7	2.5	1480	4	US-09-425-453A-18	Sequence 18, Appli	484	7	2.5	2621	3	US-08-467-902A-23	Sequence 23, Appli
412	7	2.5	1480	4	US-09-425-453A-20	Sequence 20, Appli	485	7	2.5	2621	3	US-09-275-265-23	Sequence 23, Appli
413	7	2.5	1480	4	US-08-469-630-17	Sequence 17, Appli	486	7	2.5	2621	4	US-09-941-611-23	Sequence 23, Appli
414	7	2.5	1480	4	US-09-949-016-5949	Sequence 5949, Ap	487	7	2.5	2621	4	US-08-443-260-3	Sequence 3, Appli
415	7	2.5	1480	5	PCT-US93-11667-2	Sequence 2, Appli	488	7	2.5	2621	2	US-08-442-805A-3	Sequence 3, Appli
416	7	2.5	1480	5	Patent No. 5240846	Sequence 2, Appli	489	7	2.5	2621	3	US-08-443-900A-3	Sequence 3, Appli
417	7	2.5	1480	6	5240846-5	Patent No. 5240846	490	7	2.5	2621	3	US-08-249-843-3	Sequence 3, Appli
418	7	2.5	1480	6	US-09-949-016-11311	Sequence 11311, A	491	7	2.5	2621	3	US-08-444-818-138	Sequence 138, App
419	7	2.5	1501	4	US-08-463-092B-7	Sequence 7, Appli	492	7	2.5	2621	3	US-08-324-977-2	Sequence 2, Appli
420	7	2.5	1548	1	US-08-460-907B-7	Sequence 7, Appli	493	7	2.5	2621	3	US-08-324-977-14	Sequence 14, Appli
421	7	2.5	1548	2	US-08-188-281B-12	Sequence 12, Appli	494	7	2.5	2621	1	US-08-384-616-2	Sequence 2, Appli
422	7	2.5	1648	1	US-08-188-281B-12	Sequence 12, Appli	495	7	2.5	2621	2	US-08-384-616-14	Sequence 14, Appli
423	7	2.5	1648	5	PCT-US94-07280-12	Sequence 12, Appli	496	7	2.5	2621	2	US-08-384-616-14	Sequence 2, Appli
424	7	2.5	1648	5	PCT-US95-01087-12	Sequence 12, Appli	497	7	2.5	2621	2	US-08-904-686A-14	Sequence 14, Appli
425	7	2.5	1692	3	US-09-263-933-4	Sequence 4, Appli	498	7	2.5	2621	2	US-08-315-850-2	Sequence 2, Appli
426	7	2.5	1692	3	US-09-263-933-11	Sequence 11, Appli	499	7	2.5	2621	3	US-09-014-416-3	Sequence 3, Appli
427	7	2.5	1692	3	US-09-263-933-18	Sequence 18, Appli	500	7	2.5	2621	3	US-09-315-850-14	Sequence 14, Appli
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429	7	2.5	1692	4	US-09-919-901-11	Sequence 11, Appli	502	7	2.5	2621	4	US-09-539-601-21	Sequence 21, Appli
430	7	2.5	1692	4	US-09-919-901-18	Sequence 18, Appli	503	7	2.5	2621	4	US-09-539-601-27	Sequence 27, Appli
431	7	2.5	1692	4	US-10-191-966-4	Sequence 4, Appli	504	7	2.5	2621	4	US-09-539-601-33	Sequence 33, Appli
432	7	2.5	1692	4	US-10-191-966-11	Sequence 11, Appli	505	7	2.5	2621	4	US-08-188-281B-1	Sequence 1, Appli
433	7	2.5	1692	4	US-10-191-966-18	Sequence 18, Appli	506	7	2.5	2621	1	US-08-453-552-1	Sequence 1, Appli
434	7	2.5	1786	3	US-08-444-818-54	Sequence 54, Appli	507	7	2.5	2621	1	US-08-453-552-2	Sequence 2, Appli
435	7	2.5	1985	4	US-09-539-601-9	Sequence 9, Appli	508	7	2.5	2621	1	US-08-440-103-36	Sequence 36, Appli
436	7	2.5	1985	4	US-09-539-601-12	Sequence 12, Appli	509	7	2.5	2621	1	US-08-440-542-36	Sequence 36, Appli
437	7	2.5	1985	4	US-09-539-601-18	Sequence 18, Appli	510	7	2.5	2621	1	US-07-910-760-10	Sequence 10, Appli
438	7	2.5	1985	4	US-09-539-601-24	Sequence 24, Appli	511	7	2.5	2621	1	US-08-440-519-10	Sequence 10, Appli
439	7	2.5	1985	4	US-09-539-601-30	Sequence 30, Appli	512	7	2.5	2621	1	US-08-231-368-36	Sequence 36, Appli
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441	7	2.5	2013	2	US-08-384-616-12	Sequence 12, Appli	514	7	2.5	2621	2	US-08-710-637-1	Sequence 1, Appli
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443	7	2.5	2013	3	US-09-315-850-12	Sequence 12, Appli	516	7	2.5	2621	2	US-08-833-678A-6	Sequence 6, Appli
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447	7	2.5	2201	4	US-09-539-601-15	Sequence 15, Appli	520	7	2.5	2621	3	US-09-014-416-5	Sequence 5, Appli
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459	7	2.5	2307	3	US-08-263-933-9	Sequence 9, Appli	532	7	2.5	2621	5	PCT-US93-00907-1	Sequence 1, Appli
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573	6	2.2	49	1	US-08-548-540-97	Sequence 97, Appl	646	6	2.2	109	3	US-08-469-617-26	Sequence 26, Appl
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576	6	2.2	49	1	US-08-548-540-103	Sequence 103, App	649	6	2.2	110	3	US-08-469-617-30	Sequence 30, Appl
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582	6	2.2	49	5	PCT-US96-09809-99	Sequence 99, Appl	655	6	2.2	111	1	US-08-466-886-41	Sequence 35, Appl
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715	6	2.2	160	4	US-09-647-140B-24	Sequence 24, Appl1	788	221	4	Sequence 7824, Ap	Sequence 7824, Ap
716	6	2.2	161	4	US-09-647-140B-30	Sequence 30, Appl1	789	222	4	Sequence 3641, Ap	Sequence 3641, Ap
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718	6	2.2	163	4	US-09-647-140B-2	Sequence 2, Appl1	791	224	4	Sequence 11235, A	Sequence 11235, A
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729	6	2.2	174	4	US-09-107-433-2826	Sequence 2826, Ap	802	235	4	Sequence 358, App	Sequence 358, App
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733	6	2.2	178	4	US-09-614-912-134	Sequence 134, App	806	239	4	Sequence 298, App	Sequence 298, App
734	6	2.2	179	4	US-09-583-110-2697	Sequence 2697, Ap	807	240	4	Sequence 300, App	Sequence 300, App
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738	6	2.2	183	4	US-09-902-540-11559	Sequence 11559, A	811	244	4	Sequence 3215, Ap	Sequence 3215, Ap
739	6	2.2	184	4	US-09-107-433-2989	Sequence 2989, Ap	812	245	4	Sequence 17365, A	Sequence 17365, A
740	6	2.2	185	4	US-09-489-039A-7327	Sequence 7327, Ap	813	246	4	Sequence 5486, Ap	Sequence 5486, Ap
741	6	2.2	186	4	US-09-902-540-10400	Sequence 10400, A	814	247	4	Sequence 7167, Ap	Sequence 7167, Ap
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748	6	2.2	193	4	US-09-252-991A-19743	Sequence 19743, A	821	254	4	Sequence 3452, Ap	Sequence 3452, Ap
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757	6	2.2	202	4	US-08-450-482B-89	Sequence 89, Appl1	830	263	4		

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842	6	2.2	235	4	US-09-198-452A-752	Sequence 752, App	915	2.2	255	4	US-09-493-681A-6727	Sequence 6727, App
843	6	2.2	235	4	US-09-689-065B-4	Sequence 4, Appli	916	2.2	255	4	US-09-107-433-3563	Sequence 3563, App
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846	6	2.2	235	4	US-09-438-185A-710	Sequence 710, App	919	2.2	256	4	US-09-107-433-4151	Sequence 4151, App
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880	6	2.2	247	4	US-09-134-000C-4300	Sequence 4300, App	953	2.2	266	4	US-09-538-092-313	Sequence 313, App
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991 6 2.2 280 3 US-09-307-925-15 Sequence 15, Appl
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993 6 2.2 280 4 US-09-991-582B-15 Sequence 15, Appl
994 6 2.2 280 4 US-09-107-433-3310 Sequence 3310, Ap
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996 6 2.2 281 4 US-09-489-039A-9637 Sequence 9637, Ap
997 6 2.2 281 4 US-09-489-039A-12504 Sequence 12504, A
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ALIGNMENTS

RESULT 1
US-09-583-110-4380
; Sequence 4380, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics
; CURRENT FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4380
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4380

Query Match 95.7%; Score 267; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e-258;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-107-433-4838
; Sequence 4838, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4838:

SEQUENCE CHARACTERISTICS:

LENGTH: 280 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...280

SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

US-09-107-433-4838

Query Match 95.7%; Score 267; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.6e-258;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 242 EVQLGVPKITAFCKRLADRGVSPKRLP 268

RESULT 3
US-09-214-307A-2
; Sequence 2, Application US/09214307A
; Patent No. 6544516
; GENERAL INFORMATION:
; APPLICANT: NEUTEC PHARMA PLC
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF INFECTIONS OF GRAM POSITIVE
; FILE REFERENCE: COCCI
; CURRENT APPLICATION NUMBER: US/09/214,307A
; PRIOR FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01830
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: GB9614274.0
; PRIOR FILING DATE: 1996-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-09-214-307A-2

Query Match 6.5%; Score 18; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 141 RSPFELSGGQMRRAIAG 158
Db 145 RSPFELSGGQMRRAIAG 162

RESULT 4
US-09-107-532A-6030
; Sequence 6030, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arianello, Pamela Deneke
; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6030:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...284
; SEQUENCE DESCRIPTION: SEQ ID NO: 6030:
US-09-107-532A-6030
Query Match 6.5%; Score 18; DB 4; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 141 RSPFELSGGQMRRAIAG 158
Db 152 RSPFELSGGQMRRAIAG 169

RESULT 5
US-09-134-000C-4732
; Sequence 4732, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4732
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4732

Query Match 6.1%; Score 17; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 142 SPFELSGGQMRRAIAG 158
Db 169 SPFELSGGQMRRAIAG 185

RESULT 6
US-09-861-451A-42
; Sequence 42, Application US/09861451A
; Patent No. 6759516
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific & Industrial Research Orga
; TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences
; FILE REFERENCE: PF34033/01
; CURRENT APPLICATION NUMBER: US/09/861,451A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PF273
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42


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; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Deduced protein
; OTHER INFORMATION: sequence from clone pAD913
US-09-861-451A-42
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Query Match          3.9%; Score 11; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 152 RRVATAGILAM 162
    |||||
DB 165 RRVATAGILAM 175
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RESULT 7
US-10-162-012-36
; Sequence 36, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 198
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-162-012-36
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Query Match          3.6%; Score 10; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 169 LDEPTAGLDP 178
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DB 146 LDEPTAGLDP 155
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RESULT 8
US-09-489-039A-10009
; Sequence 10009, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10009
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10009
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Query Match          3.6%; Score 10; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 169 LDEPTAGLDP 178
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DB 167 LDEPTAGLDP 176
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RESULT 9
US-09-134-001C-3292
; Sequence 3292, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3292
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3292
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Query Match          3.6%; Score 10; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 169 LDEPTAGLDP 178
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DB 171 LDEPTAGLDP 180
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; APPLICANT: Pompejus, Mark
; APPLICANT: Kr"ger, Burkhard
; APPLICANT: Sch"der, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5

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; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 352
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-787A-352

Query Match          3.6%; Score 10; DB 4; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDP 178
DB 150 LDEPTAGLDP 159

RESULT 11
US-09-252-991A-21585
; Sequence 21585, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21585
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21585

Query Match          3.6%; Score 10; DB 4; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDP 178
DB 525 LDEPTAGLDP 534

RESULT 12
US-09-902-540-14362
; Sequence 14362, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B

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; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14362
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14362

Query Match 3.2%; Score 9; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 170 DEPTAGLDP 178
Db 159 DEPTAGLDP 167
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RESULT 13

US-09-489-039A-9627
; Sequence 9627, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9627
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9627

Query Match 3.2%; Score 9; DB 4; Length 546;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 EPAILVLDE 171
Db 445 EPAILVLDE 453
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RESULT 14

US-09-543-681A-6008
; Sequence 6008, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:

; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6008
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6008

Query Match 3.2%; Score 9; DB 4; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GHTSGKST 48
Db 379 GHTSGKST 387
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RESULT 15

US-09-489-039A-13507
; Sequence 13507, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13507
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13507

Query Match 3.2%; Score 9; DB 4; Length 686;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GHTSGKST 48
Db 468 GHTSGKST 476
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Search completed: October 28, 2005, 18:15:42
Job time : 58 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-09-769-744D-26

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1378	99.4	279	9	US-10-617-320-4838
5	1378	99.4	279	15	US-09-815-242-13440
6	1002.5	72.3	280	15	US-10-282-122A-74238
7	971	70.0	280	15	US-10-282-122A-74238
8	850.5	61.3	289	9	US-10-282-122A-74821
9	850.5	61.3	289	15	US-10-282-122A-74821
10	845.5	61.0	289	15	US-10-282-122A-74821
11	794	57.2	232	18	US-10-501-282-342

12	794	57.2	294	18	US-10-501-282-344	Sequence 344, App
13	729	52.6	276	15	US-10-369-493-23054	Sequence 23054, A
14	700	50.5	293	15	US-10-282-122A-46693	Sequence 46693, A
15	692.5	49.9	288	15	US-10-282-122A-60478	Sequence 60478, A
16	683	49.2	288	15	US-10-282-122A-51996	Sequence 51996, A
17	661	47.7	288	15	US-10-282-122A-52691	Sequence 52691, A
18	637.5	46.0	282	15	US-10-369-493-17105	Sequence 17105, A
19	635.5	45.8	288	15	US-10-282-122A-53490	Sequence 53490, A
20	611	44.1	286	15	US-10-282-122A-71161	Sequence 71161, A
21	608	43.8	288	18	US-10-724-972A-6429	Sequence 6429, Ap
22	607	43.8	286	15	US-10-282-122A-71345	Sequence 71345, A
23	594.5	42.9	286	9	US-09-815-242-12234	Sequence 12234, A
24	589.5	42.5	286	15	US-10-282-122A-44395	Sequence 44395, A
25	589.5	42.5	286	17	US-10-857-625-742	Sequence 742, App
26	553	39.9	272	15	US-10-282-122A-45314	Sequence 45314, A
27	548.5	39.5	273	9	US-09-815-242-5550	Sequence 5550, Ap
28	543	39.1	180	14	US-10-054-968-2	Sequence 2, Appli
29	540.5	39.0	304	15	US-10-282-122A-63497	Sequence 63497, A
30	533.5	38.5	303	15	US-10-282-122A-64291	Sequence 64291, A
31	508	36.6	300	9	US-09-861-451A-42	Sequence 42, Appli
32	489.5	35.3	277	15	US-10-282-122A-53483	Sequence 53483, A
33	486	35.0	273	15	US-10-369-493-16472	Sequence 16472, A
34	485	35.0	279	15	US-10-282-122A-52131	Sequence 52131, A
35	484.5	34.9	285	15	US-10-282-122A-52539	Sequence 52539, A
36	484	34.9	300	15	US-10-282-122A-45307	Sequence 45307, A
37	483.5	34.9	281	15	US-10-282-122A-52154	Sequence 52154, A
38	479	34.5	279	15	US-10-282-122A-60654	Sequence 60654, A
39	468.5	33.8	279	15	US-10-282-122A-57649	Sequence 57649, A
40	457	32.9	433	15	US-10-282-122A-76895	Sequence 76895, A
41	454.5	32.8	279	15	US-10-282-122A-57249	Sequence 57249, A
42	454.5	32.8	291	9	US-09-815-242-10544	Sequence 10544, A
43	452	32.6	279	18	US-10-501-282-346	Sequence 346, App
44	431.5	31.1	274	15	US-10-282-122A-64292	Sequence 64292, A
45	424.5	30.6	296	15	US-10-282-122A-74822	Sequence 74822, A

ALIGNMENTS

RESULT 1

US-09-769-744A-26
; Sequence 26, Application US/09769744A
; Publication No. US20030134407A1
; GENERAL INFORMATION:
; APPLICANT: Le Page, Richard WF
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hanniffy, Sean B
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21122WO
; CURRENT APPLICATION NUMBER: US/09/769, 744A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/GB99/02452
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: GB 9816336.3
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/125329
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-744A-26

Query Match 100.0%; Score 1387; DB 10; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.1e-122;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MGIALENVNTYQEGTPTLASAALSDVSLTDCSYTALIGHTSGKSTIQLNGLLVPS 60
1 MGIALENVNTYQEGTPTLASAALSDVSLTDCSYTALIGHTSGKSTIQLNGLLVPS 60

QY 61 QGSRVFDLTITSTSKNDIRQIRKQVGLVFOFAENQIFEEETVLKDVAFGPNFGVSEED 120
DB 61 QGSRVFDLTITSTSKNDIRQIRKQVGLVFOFAENQIFEEETVLKDVAFGPNFGVSEED 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDPTAGLDPLG 180
DB 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDPTAGLDPLG 180
QY 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGLVKGKPSDFQDVVFWME 240
DB 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGLVKGKPSDFQDVVFWME 240
QY 241 EVQLGVPKITAFCKRLADRGVSKRLPIKIEFKESLNG 279
DB 241 EVQLGVPKITAFCKRLADRGVSKRLPIKIEFKESLNG 279

RESULT 2

US-10-472-928-4660
; Sequence 4660, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926W0
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4660
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: ABC transporter, ATP-binding protein
; OTHER INFORMATION: Cellular location: membrane
; OTHER INFORMATION: Similar to strain R6 sequence 15904066 (e-154)
US-10-472-928-4660

Query Match 100.0%; Score 1387; DB 17; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.1e-122;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIALENVNTYQSGTPLASALSDVSLTIEDGSYTALIGHTGSGKSTILQLLNGLLVPS 60
DB 1 MGIALENVNTYQSGTPLASALSDVSLTIEDGSYTALIGHTGSGKSTILQLLNGLLVPS 60
QY 61 QGSRVFDLTITSTSKNDIRQIRKQVGLVFOFAENQIFEEETVLKDVAFGPNFGVSEED 120
DB 61 QGSRVFDLTITSTSKNDIRQIRKQVGLVFOFAENQIFEEETVLKDVAFGPNFGVSEED 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDPTAGLDPLG 180
DB 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDPTAGLDPLG 180
QY 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGLVKGKPSDFQDVVFWME 240
DB 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGLVKGKPSDFQDVVFWME 240
QY 241 EVQLGVPKITAFCKRLADRGVSKRLPIKIEFKESLNG 279
DB 241 EVQLGVPKITAFCKRLADRGVSKRLPIKIEFKESLNG 279

RESULT 3

US-10-617-320-4838
; Sequence 4838, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,320
FILING DATE: 10-Jul-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4838:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...280
SEQUENCE DESCRIPTION: SEQ ID NO: 4838:
US-10-617-320-4838

Query Match 99.9%; Score 1386; DB 18; Length 280;
Best Local Similarity 99.6%; Pred. No. 2.6e-122;
Matches 278; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIALENVNTYQSGTPLASALSDVSLTIEDGSYTALIGHTGSGKSTILQLLNGLLVPS 60
DB 2 MGIALENVNTYQSGTPLASALSDVSLTIEDGSYTALIGHTGSGKSTILQLLNGLLVPS 61
QY 61 QGSRVFDLTITSTSKNDIRQIRKQVGLVFOFAENQIFEEETVLKDVAFGPNFGVSEED 120
DB 62 QGSRVFDLTITSTSKNDIRQIRKQVGLVFOFAENQIFEEETVLKDVAFGPNFGVSEED 121
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDPTAGLDPLG 180
DB 122 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDPTAGLDPLG 181
QY 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGLVKGKPSDFQDVVFWME 240
DB 182 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGLVKGKPSDFQDVVFWME 241
QY 241 EVQLGVPKITAFCKRLADRGVSKRLPIKIEFKESLNG 279
DB 242 EVQLGVPKITAFCKRLADRGVSKRLPIKIEFKESLNG 280

RESULT 4

US-09-815-242-13440

; Sequence 13440, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: Fast-SEQ for Windows Version 4.0

; SEQ ID NO 13440

; LENGTH: 279

; TYPE: PRF

; ORGANISM: Streptococcus pneumoniae

US-09-815-242-13440

Query Match 99.4%; Score 1378; DB 9; Length 279;

Best Local Similarity 99.3%; Pred. No. 1.5e-121;

Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGIALENNVFTYQEGTPLASAAALSDVSLTIEDGSGYALIGHTGSGKSTILQINGLLVPS 60

Db 1 MGIALENNVFTYQEGTPLASAAALSDVSLTIEDGSGYALIGHTGSGKSTILQINGLLVPS 60

Qy 61 QGSVRVPDTLITSTSKNKDIQIRKQVGLVQFAENQIPEETVLKDVAFQPNFGVSEED 120

Db 61 QGSVRVPDTLITSTSKNKDIQIRKQVGLVQFAENQIPEETVLKDVAFQPNFGVSEED 120

Qy 121 AVKTAREKALVGDLSLDFRSPFELSGGOMRRAVAIAGILAMEPAILVLDEPTAGLDPLG 180

Db 121 AVKTAREKALVGDLSLDFRSPFELSGGOMRRAVAIAGILAMEPAILVLDEPTAGLDPLG 180

Qy 181 RKELMTLTKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRVLKGGKPSDVFQDVVFWME 240

Db 181 RKELMTLTKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRVLKGGKPSDVFQDVVFWME 240

Qy 241 EVQLGVPKITAFCCKRLADRGVSPKRLPIKIEEFKESLNG 279

Db 241 EVQLGVPKITAFCCKRLADRGVSPKRLPIKIEEFKESLNG 279

RESULT 5

US-10-282-122A-74238

; Sequence 74238, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 74238

LENGTH: 279

TYPE: PRF

ORGANISM: Streptococcus pneumoniae

US-10-282-122A-74238

Query Match 99.4%; Score 1378; DB 15; Length 279;

Best Local Similarity 99.3%; Pred. No. 1.5e-121;

Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGIALENNVFTYQEGTPLASAAALSDVSLTIEDGSGYALIGHTGSGKSTILQINGLLVPS 60

Db 1 MGIALENNVFTYQEGTPLASAAALSDVSLTIEDGSGYALIGHTGSGKSTILQINGLLVPS 60

Qy 61 QGSVRVPDTLITSTSKNKDIQIRKQVGLVQFAENQIPEETVLKDVAFQPNFGVSEED 120

Db 61 QGSVRVPDTLITSTSKNKDIQIRKQVGLVQFAENQIPEETVLKDVAFQPNFGVSEED 120

Qy 121 AVKTAREKALVGDLSLDFRSPFELSGGOMRRAVAIAGILAMEPAILVLDEPTAGLDPLG 180

Db 121 AVKTAREKALVGDLSLDFRSPFELSGGOMRRAVAIAGILAMEPAILVLDEPTAGLDPLG 180

Qy 181 RKELMTLTKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRVLKGGKPSDVFQDVVFWME 240

Db 181 RKELMTLTKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRVLKGGKPSDVFQDVVFWME 240

Qy 241 EVQLGVPKITAFCCKRLADRGVSPKRLPIKIEEFKESLNG 279

Db 241 EVQLGVPKITAFCCKRLADRGVSPKRLPIKIEEFKESLNG 279

RESULT 6

US-10-282-122A-72498

; Sequence 72498, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

```
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72498
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-282-122A-72498

Query Match      72.3%; Score 1002.5; DB 15; Length 280;
Best Local Similarity 70.0%; Pred. No. 4.4e-86;
Matches 196; Conservative 38; Mismatches 45; Indels 1; Gaps 1;

QY 1 MGIALENVFTYQGTPLASAAALSDVSLTIEDGYSYTAUGHTGSGKSTILQLLNGLLVPS 60
DB 1 MGINLQVSVTYQAGTPPEGRALFNVSLEIKDGSFTAFIGHTGSGKSTIMQLLNGLTPT 60
QY 61 QGSVRVFTLTSTSKNDIROIKQVGLVFOFAENQIFETVLKDVAFGPNFGVSEED 120
DB 61 EGTVLVDVATRSKNDIROIKRVKGLVFOFPESQLFDETVLKDVAFGPNFGVSKEE 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRVAIAGILAMEPAAILVLDEPTAGLDPLG 180
DB 121 AEKLAEREKALVIGISEELFEKNPFELSGQMRVAIAGILAMEPILVLDEPTAGLDPKG 180
QY 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRVLKGGKPSDFQDVVPM 240
DB 181 RRELMTLFPKLLHQSGMTIVLVTHLMDVSNYADVYVLEKGRVLKGGKPSDFQDVVPM 240
QY 241 EVQLGVPKITAFCKRLADRGVSKFLPIKIEEFKESL-NG 279
DB 241 SKQLGVPKITQFAHLREKGTIFDALPITLBEFVEAKNG 280
```

RESULT 7

US-10-282-122A-74821

; Sequence 74821, Application US/10282122A

```
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74821
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74821

Query Match      70.0%; Score 971; DB 15; Length 280;
Best Local Similarity 69.0%; Pred. No. 4.2e-83;
Matches 191; Conservative 35; Mismatches 51; Indels 0; Gaps 0;

QY 1 MGIALENVFTYQGTPLASAAALSDVSLTIEDGYSYTAUGHTGSGKSTILQLLNGLLVPS 60
DB 1 MSINLQVSVTYQAGTPPEGRALFNINLIDGYSYTAUGHTGSGKSTIMQLLNGLVPT 60
QY 61 QGSVRVFTLTSTSKNDIROIKQVGLVFOFAENQIFETVLKDVAFGPNFGVSEED 120
DB 61 TGISVVDKQDITNHSKNDIROIKRVKGLVFOFPESQLFDETVLKDVAFGPNFGVSEED 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRVAIAGILAMEPAAILVLDEPTAGLDPLG 180
DB 121 AEALAREKALVIGISEELFEKNPFELSGQMRVAIAGILAMEPILVLDEPTAGLDPKG 180
QY 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRVLKGGKPSDFQDVVPM 240
DB 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRVLKGGKPSDFQDVVPM 240
QY 241 EVQLGVPKITAFCKRLADRGVSKFLPIKIEEFKESL 277
DB 241 KKQLGVPKVTKLAORLVDRGIPITSSLPITLBELEVL 277
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RESULT 8

US-09-815-242-10545	
; Sequence 10545, Application US/09815242	
; Patent No. US20020061569A1	
; GENERAL INFORMATION:	
; APPLICANT: Haselbeck, Robert	
; APPLICANT: Ohlsen, Kari L.	
; APPLICANT: Zyskind, Judith W.	
; APPLICANT: Wall, Daniel	
; APPLICANT: Trawick, John D.	
; APPLICANT: Carr, Grant J.	
; APPLICANT: Yamamoto, Robert T.	
; APPLICANT: Xu, H. Howard	
; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes	
; FILE REFERENCE: ELITRA.011A	
; CURRENT APPLICATION NUMBER: US/09/815,242	
; CURRENT FILING DATE: 2001-03-21	
; PRIOR APPLICATION NUMBER: 60/191,078	
; PRIOR FILING DATE: 2000-03-21	
; PRIOR APPLICATION NUMBER: 60/206,848	
; PRIOR FILING DATE: 2000-05-23	
; PRIOR APPLICATION NUMBER: 60/207,727	
; PRIOR FILING DATE: 2000-05-26	
; PRIOR APPLICATION NUMBER: 60/242,578	
; PRIOR FILING DATE: 2000-10-23	
; PRIOR APPLICATION NUMBER: 60/253,625	
; PRIOR FILING DATE: 2000-11-27	
; PRIOR APPLICATION NUMBER: 60/257,931	
; PRIOR FILING DATE: 2000-12-22	
; PRIOR APPLICATION NUMBER: 60/269,308	
; PRIOR FILING DATE: 2001-02-16	
; NUMBER OF SEQ ID NOS: 1410	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 10545	
; LENGTH: 289	
; TYPE: PRT	
; ORGANISM: Enterococcus faecalis	
US-09-815-242-10545	
Query Match 61.3%; Score 850.5; DB 9; Length 289;	
Best Local Similarity 57.9%; Pred. No. 1.1e-71;	
Matches 161; Conservative 54; Mismatches 62; Indels 1; Gaps 1;	
QY 1	MGIALENVFTYQEGTPLASALSDVSLTEDGSYTALICHTGSGKSTIOLLNGLVPS 60
DB 1	MDIRFKQVDFTYQNTPFQEQALFDINLTQDGSYTAIVGHTGSGKSTLLQHLNALVKPT 60
QY 61	QGSVRVFDTLTSTSKNKDIQIRKQVGLVFPQFAENQIPEETVLKDVAFQPNFGVSEED 120
DB 61	KQVVTIGERVITPETDNKNLKPIRKKVGIVFPQPEAQLFEETVERDIAFGPKNFGVSD 120
QY 121	AVKTAREKALVGDIDSLFDRSPFELSGGQMRRAVAIAGILAMEPAIILVLDDEPTAGLDPLG 180
DB 121	AKKLAKMOLDVLGDEKYLQHSFPFELSGGQMRRAVAIAGVLAWEPEVLVLDDEPTAGLDPKG 180
QY 181	RKELMTLFFKLH-QSGMTIVLVTHLMDDDVAEYANOVYVMEKGRLYKGGKPSDVFDVVF 239
DB 181	RKEMMEMFSRLHKEHNNTIVLVTHLMDDDVANYADHVILEKQIVVRAGAPQEVFQETQWL 240
QY 240	EEVOLGVPKITAFCKRLADRGVSFKRLPIKIEBFKESL 277
DB 241	KEKQLGVPTAAEFAEKLVAKGFSFEQLPLTADQLADQL 278
RESULT 9	
US-10-282-122A-57248	
; Sequence 57248, Application US/10282122A	
; Publication No. US20040029129A1	
; GENERAL INFORMATION:	
; APPLICANT: Wang, Liangsu	
; APPLICANT: Zamudio, Carlos	
; APPLICANT: Malone, Cheryl	
; APPLICANT: Haselbeck, Robert	
US-10-282-122A-57248	
Query Match 61.3%; Score 850.5; DB 15; Length 289;	
Best Local Similarity 57.9%; Pred. No. 1.1e-71;	
Matches 161; Conservative 54; Mismatches 62; Indels 1; Gaps 1;	
QY 1	MGIALENVFTYQEGTPLASALSDVSLTEDGSYTALICHTGSGKSTIOLLNGLVPS 60
DB 1	MDIRFKQVDFTYQNTPFQEQALFDINLTQDGSYTAIVGHTGSGKSTLLQHLNALVKPT 60
QY 61	QGSVRVFDTLTSTSKNKDIQIRKQVGLVFPQFAENQIPEETVLKDVAFQPNFGVSEED 120
DB 61	KQVVTIGERVITPETDNKNLKPIRKKVGIVFPQPEAQLFEETVERDIAFGPKNFGVSD 120
QY 121	AVKTAREKALVGDIDSLFDRSPFELSGGQMRRAVAIAGILAMEPAIILVLDDEPTAGLDPLG 180
DB 121	AKKLAKMOLDVLGDEKYLQHSFPFELSGGQMRRAVAIAGVLAWEPEVLVLDDEPTAGLDPKG 180
QY 181	RKELMTLFFKLH-QSGMTIVLVTHLMDDDVAEYANOVYVMEKGRLYKGGKPSDVFDVVF 239
DB 181	RKEMMEMFSRLHKEHNNTIVLVTHLMDDDVANYADHVILEKQIVVRAGAPQEVFQETQWL 240
QY 240	EEVOLGVPKITAFCKRLADRGVSFKRLPIKIEBFKESL 277
DB 241	KEKQLGVPTAAEFAEKLVAKGFSFEQLPLTADQLADQL 278
RESULT 10	
US-10-282-122A-57659	
; Sequence 57659, Application US/10282122A	
; Publication No. US20040029129A1	
; GENERAL INFORMATION:	
; APPLICANT: Wang, Liangsu	
; APPLICANT: Zamudio, Carlos	
; APPLICANT: Zamudio, Carlos	

```
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57659
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57659

Query Match 61.0%; Score 845.5; DB 15; Length 289;
Best Local Similarity 58.3%; Pred. No. 3.1e-71;
Matches 162; Conservative 53; Mismatches 62; Indels 1; Gaps 1;

Qy 1 MGIALENVNTYQEGTPLASALSVDLSLTIEDGYSYALIGHTGSKSTILQLLGLLVPS 60
Db 1 MDIRPEQVDFTYQNPTEQRALPDINMTIKENSYVALVGHGTSKSTILQLLGLLVKPT 60

Qy 61 QGSVRVFTLTSTSKNDIRQIRKQVGLVQPAENQIPBETVLKDVAFGPNFGVSEED 120
Db 61 SGTVHIGERDIPQTDNKNLKPIRKKGIVGFQPEAQLFEETVANDIAFGPKNFGVSEE 120

Qy 121 AVKTAREKIALVGDIESLFDSPPELGGQRRVAIGILAMEPAILVLDSEPTAGLDPLG 180
Db 121 ALVLAKETLEQGLDESYLESPPELGGQRRVAIGVLAWRPVLVDSEPTAGLDPLG 180

Qy 181 RKELMTLTKKLH-QSGMTIVLTVHLMDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFM 239
Db 181 RKENMEMPRWLKHEQQIITVLTVHLMDDVANPADVYVYVLEKGRIVNSGEPQEVFNIEWL 240

Qy 240 BEVQLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
Db 241 KEKQLGVPTATSFABELMAKGNFATLPLTABELADAI 278

RESULT 11
US-10-501-282-342
; Sequence 342, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOLOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 344
; LENGTH: 294
; TYPE: PRT
```

```
; APPLICANT: MCMICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOLOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 342
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Alloiococcus otitidis
US-10-501-282-342

Query Match 57.2%; Score 794; DB 18; Length 292;
Best Local Similarity 54.1%; Pred. No. 2.3e-66;
Matches 151; Conservative 62; Mismatches 64; Indels 2; Gaps 2;

Qy 1 MGIALENVNTYQEGTPLASALSVDLSLTIEDGYSYALIGHTGSKSTILQLLGLLVPS 60
Db 1 MDIRPEQVGFYQKTPESRALYDINLSIKGYSYVALVGHGTSKSTVLQHLNALKIPT 60

Qy 61 QGSVRVFTLTSTSKNDIRQIRKQVGLVQPAENQIPBETVLKDVAFGPNFGVSEED 120
Db 61 EGQVHIGDRVISQESENKKALKRKGIVGFQPEAQLFEETVQGDIAFGPKNFGKQSEE 120

Qy 121 AVKTAREKIALVGDIESLFDSPPELGGQRRVAIGILAMEPAILVLDSEPTAGLDPLG 180
Db 121 ADDIVQDMLLVGLDESFRDRSPDLGGQRRVAIGVLAQEVVLVDSEPTAGLDPLG 180

Qy 181 RKELMTLTKKLH-QSGMTIVLTVHLMDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFM 239
Db 181 RQETMDMFPYKLHKEGLTIVLVTHQMEDVADYADHMTIVLDHGTVKREGQPREIFKEADWL 240

Qy 240 BEVQLGVPKITAFCKRL-ADRGVSFKRLPIKIEEFKESL 277
Db 241 NSLKLGLPKSVRFANRLQKSEFGWDFDLPLTTEELGQAI 279

RESULT 12
US-10-501-282-344
; Sequence 344, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOLOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 344
; LENGTH: 294
; TYPE: PRT
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; ORGANISM: Alloiococcus otitidis
US-10-501-282-344

Query Match      57.2%; Score 794; DB 18; Length 294;
Best Local Similarity 54.1%; Pred. No. 2.4e-66;
Matches 151; Conservative 62; Mismatches 64; Indels 2; Gaps 2;

QY 1 MGIALENVFTYQEGTTPLASAALSDVSLTIEDGSGYALIGHTSGKSTILQLLNGLLVPS 60
DB 3 MDIRFOEVGFTYQKGTFFESRALYDINLSIKDGSYALVGHGTSGKSTVQLHNAIKFT 62

QY 61 QGSVRVFDTLTSTSKNKDIQRIKQVGLVFOFAENQIPEETVLKDVAFGPQNFVSEED 120
DB 63 EQQVHIGDRVISOESENKKLALKRKKVGVVFQPEAQLFEETVGDIAFGPKNFGKSQE 122

QY 121 AVKTAREKALVIGIDESLFDSPFELSGGQRRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
DB 123 ADDIVQDMLLVGLDESFRDRSPFDLSGGQRRVAIAGVLAQPEVLVLDDEPTAGLDPKG 182

QY 181 RKELMTLFFKKLH-QSGMTIVLVTHLMDVVAEYANQVYVMEKGRVYKGGKPSDVFDQVFM 239
DB 183 ROEIMDMFYKLHKEEGLTIVLTHQMEDVADYADHVMIVLDHGTVRKGGQPRIFREADWL 242

QY 240 BEVOLGVRPIKTAFCRKL-ADRGVSFKRLPIKIEEFKESL 277
DB 243 NSLKLGLPKSVRFANRLQKEFGWDFDLPLTTEELQAI 281

RESULT 13
US-10-369-493-23054
; Sequence 23054, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianning
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23054
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23054

Query Match      52.6%; Score 729; DB 15; Length 276;
Best Local Similarity 56.4%; Pred. No. 3e-60;
Matches 146; Conservative 45; Mismatches 66; Indels 2; Gaps 2;

QY 16 TPLAALSADVSTIEDGSGYALIGHTSGKSTILQLLNGLLVPSQGSVRVFTLTST 75
DB 3 TPERLALYDINASIKESGVAVIGHTSGKSTILQHLNGLLKPTKGQISLGSVTIQAGK 62

QY 76 KNKDIQRIKQVGLVFOFAENQIPEETVLKDVAFGPQNFVSEEDAVKTAREKALVIGID 135
DB 63 KNKDLKKRKKVGVVFQPEHQLFEETVLKDISFGPMNFGVKEDAEQKAREMLQLVGLS 122

QY 136 ESLFDRSPFELSGGQRRVAIAGILAMEPAILVLDDEPTAGLDPLGRKELMTLFLPKLHQS 195
DB 123 EELLDRSPFELSGGQRRVAIAGVLAQPEVLVLDDEPTAGLDPRKEIMDMFVFLHQ 182

QY 196 -MTIVLVTHLMDVVAEYANQVYVMEKGRVYKGGKPSDVFDQVFMEEVQLGVPIKTAFC 254
DB 183 NLTTILVTHSMEDAAAAYADEMIVMHKGTIQASGSPRDLFLKGEEMAGWGLDLPETIKFOR 242

QY 255 RL-ADRGVSFKRLPIKIEE 272
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DB 243 HLEALGVRFNEPMLTIED 261

RESULT 14
US-10-282-122A-46693
; Sequence 46693, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46693
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46693

Query Match      50.5%; Score 700; DB 15; Length 293;
Best Local Similarity 50.4%; Pred. No. 1.8e-57;
Matches 138; Conservative 53; Mismatches 81; Indels 2; Gaps 2;

QY 1 MGIALENVFTYQEGTTPLASAALSDVSLTIEDGSGYALIGHTSGKSTILQLLNGLLVPS 60
DB 1 MEITFQKVEHRYQYKTPFERRALYDVDSPPSGGYAIIIGHTSGKSTMIQHLNGLLOPT 60

QY 61 QGSVRVFDTLTSTSKNKDIQRIKQVGLVFOFAENQIPEETVLKDVAFGPQNFVSEED 120
DB 61 NGTVQIGEHFISAGKKEKLLKRLKRVGVVFQPEHQLFEETVEKDI-CFGPTFGVSEEA 120

QY 121 AVKTAREKALVIGIDESLFDSPFELSGGQRRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
DB 121 AKQKAREAIELVLEPELLARSPELSSGGQRRVAIAGVLAQPEVLVLDDEPTAGLDPKG 180

QY 181 RKELMTLFFKKLH-QSGMTIVLVTHLMDVVAEYANQVYVMEKGRVYKGGKPSDVFDQVFM 239
DB 181 QNELMEMFYKLHKEEGLTIVLTHNMDAAKAEQIVVMHKGTIVFLQGSAAEEVFSHADEL 240
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 17:35:21 ; Search time 40 Seconds
(without alignments)
671.112 Million cell updates/sec

Title: US-09-769-744D-26
Perfect score: 1387
Sequence: 1 MGIALENVNFYQEGTPLAS.....GVSFKRLPIKIEEFKESLNG 279

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: Pirl2:.*
3: Pirl3:.*
4: Pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1387	100.0	279	2 C95259	ABC transporter, A
2	1378	99.4	279	2 F98124	hypothetical prote
3	899.5	64.9	288	2 F86659	ABC transporter AT
4	729	52.6	276	2 E69742	ABC transporter (A
5	696.5	50.2	288	2 AG1775	ABC transporter (A
6	692.5	49.9	288	2 AH1399	ABC transporter (A
7	683	49.2	286	2 F97281	ABC-type transport
8	637.5	46.0	282	2 E83670	ABC transporter (A
9	595.5	42.9	304	2 C90360	ABC transporter at
10	589.5	42.5	286	2 H90018	hypothetical prote
11	540.5	39.0	304	2 I64219	membrane transport
12	533.5	38.5	303	2 G62814	histidine transport
13	511.5	36.9	279	2 G64435	cobalt transporter A
14	485	35.0	279	2 E97068	cobalt transport (
15	484	34.9	278	2 T44412	ABC transporter (A
16	483.5	34.9	281	2 G97281	ABC-type transport
17	479	34.5	279	2 A11399	ABC transporter (A
18	473	34.1	311	2 A69095	ABC transporter (A
19	465	33.5	279	2 AH1775	ABC transporter (A
20	464	33.5	277	2 T45265	cobalt transport A
21	457.5	33.0	280	2 G69043	cobalt transporter A
22	457	32.9	433	2 D82879	ABC transporter UU
23	456.5	32.9	280	2 H75151	abc transporter, A
24	443	31.9	260	2 B71234	probable transport
25	436.5	31.5	281	2 E69751	ABC transporter (A
26	435.5	31.4	266	2 A72401	ABC transporter, A
27	431.5	31.1	274	2 S62815	sulfate transporter
28	431.5	31.1	284	2 G71192	probable cobalt tr
29	429.5	31.0	280	2 T03543	probable cobalt tr

ALIGNMENTS

RESULT 1

C95259
ABC transporter, ATP-binding protein SP2220 [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 16-Aug-2004
C;Accession: C95259
R;Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidn on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle, I nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: C95259
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <KUR>
A;Cross-references: UNIPROT:Q97N51; GB:AE005672; PIDN:AAK76268.1; PID:g14973730; GSPDB:G C;Genetics:
A;Experimental source: strain TIGR4
C;Superfamily: ATP-binding cassette homology

Query Match	100.0%;	Score 1387;	DB 2;	Length 279;
Best Local Similarity	100.0%;	Pred. No. 9.8e-97;		
Matches 279;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGIALENVNFYQEGTPLASAA	SDVSLTIEDGSGY	TALIGHTGSGKSTILQLLGLVPS 60
Db	1	MGIALENVNFYQEGTPLASAA	SDVSLTIEDGSGY	TALIGHTGSGKSTILQLLGLVPS 60
QY	61	QGSVRVPDITLITSTSKNKQIRKQVGLVFQFAENQIFETVLKDVAFQPNQGVSEED	120	
Db	61	QGSVRVPDITLITSTSKNKQIRKQVGLVFQFAENQIFETVLKDVAFQPNQGVSEED	120	
QY	121	AVKTAREKALVGDLSLDRSPFELSGGQRRVAIAGILAMEPAILLVLEDEPTAGLDPLG	180	
Db	121	AVKTAREKALVGDLSLDRSPFELSGGQRRVAIAGILAMEPAILLVLEDEPTAGLDPLG	180	
QY	181	RKELMTLTKKLHQSOGMTIVLVTHLMDDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFME	240	
Db	181	RKELMTLTKKLHQSOGMTIVLVTHLMDDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFME	240	
QY	241	EVQLGVPKITAFCRKLADRGVSFKRLPIKIEEFKESLNG	279	
Db	241	EVQLGVPKITAFCRKLADRGVSFKRLPIKIEEFKESLNG	279	

RESULT 2

F98124
hypothetical protein ABC-NBP [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 16-Aug-2004
C/Accession: F98124
R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; Mahren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Ballido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A37872; MUID:21429245; PMID:11544234
A/Accession: F98124
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-279 <KUN>
A/Cross-references: UNIPROT:Q8DMY0; GB:AE007317; PID:AA00827.1; PID:gl5459731; GSPDB:C
C/Genetics:
A/Gene: ABC-NBP
C/Superfamily: ATP-binding cassette homology

Query Match 99.4%; Score 1378; DB 2; Length 279;
Best Local Similarity 99.3%; Pred. No. 4.7e-96;
Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIALENNFTYQEGTPLASALSVDLSLTIEDGSGTALIGHTSGKSTILQNLGLLVPS 60
DB 1 MGIALENNFTYQEGTPLASALSVDLSLTIEDGSGTALIGHTSGKSTILQNLGLLVPS 60

QY 61 QGSVRVFDLTITSTSKNDIRQIRKQVGLVFPQFAENQIFETVLKDVAFGPNQFVSEED 120
DB 61 QGSVRVFDLTITSTSKNDIRQIRKQVGLVFPQFAENQIFETVLKDVAFGPNQFVSEED 120

QY 121 AVKTAREKALVIGIDESLDRSPFELSGQMRRAVIAIGLAMEPAILVLDDEPTAGLDPLG 180
DB 121 AVKTAREKALVIGIDESLDRSPFELSGQMRRAVIAIGLAMEPAILVLDDEPTAGLDPLG 180

QY 181 RKELMTLPKLLHQSGMTIVLVTHLMDVVAEYANQVVMKGRLVKGGKPSDVDFQVFWME 240
DB 181 RKELMTLPKLLHQSGMTIVLVTHLMDVVAEYANQVVMKGRLVKGGKPSDVDFQVFWME 240

QY 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
DB 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279

RESULT 3
F86659
ABC transporter ATP-binding protein ychE [imported] - Lactococcus lactis subsp. lactis
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 16-Aug-2004
C/Accession: F86659
R/Solotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A/Reference number: A86625; MUID:21235186; PMID:11337471
A/Accession: F86659
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-288 <STO>
A/Cross-references: UNIPROT:Q9CIS8; GB:AE005176; PID:gl12723140; PID:AAK04376.1; GSPDB:C
A/Experimental source: strain IL1403
C/Genetics:
A/Gene: ychE
C/Superfamily: ATP-binding cassette homology

Query Match 64.9%; Score 899.5; DB 2; Length 288;
Best Local Similarity 64.8%; Pred. No. 3.7e-60;
Matches 173; Conservative 46; Mismatches 47; Indels 1; Gaps 1;

QY 3 IALENNFTYQEGTPLASALSVDLSLTIEDGSGTALIGHTSGKSTILQNLGLLVPSQ 62
DB 2 IKFEKNVITYQNSPFASRALFDILEVKKGSYTLIGHTSGKSTILQNLGLLVPSQ 61

QY 63 SVRVFDLTITSTSKNDIRQIRKQVGLVFPQFAENQIFETVLKDVAFGPNQFVSEEDAV 122

DB 62 TVRVGDIIVTSTSKQEKIPURKKVGVVFPQPSQLEETVLKDVAFGPNQFVSEEDAV 121

QY 123 KTAREKALVIGIDESLDRSPFELSGQMRRAVIAIGLAMEPAILVLDDEPTAGLDPLGRK 182
DB 123 KTAREKALVIGIDESLDRSPFELSGQMRRAVIAIGLAMEPAILVLDDEPTAGLDPLGRK 182

QY 183 ELMTLPKLLHQSGMTIVLVTHLMDVVAEYANQVVMKGRLVKGGKPSDVDFQVFWMESEV 242
DB 183 ELMTLPKLLHQSGMTIVLVTHLMDVVAEYANQVVMKGRLVKGGKPSDVDFQVFWMESEV 242

QY 243 QLVGVPKITAFCKRLADRGV-SFKRLPI 268
DB 243 QLVGVPKITAFCKRLADRGV-SFKRLPI 268

RESULT 4
B69742
ABC transporter (ATP-binding protein) homolog ybaE - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C/Accession: B69742
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapido, A.; Lardinois,
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogilwa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptratr, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A/Authors: Yoshikawa, H.P.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: B69742
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-276 <KUN>
A/Cross-references: UNIPROT:P70970; GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11922.1
A/Experimental source: strain 168
C/Genetics:
A/Gene: ybaE
C/Superfamily: ATP-binding cassette homology
C/Keywords: ATP; nucleotide binding; P-loop
F:10-209/Domain: ATP-binding cassette homology <ABC>
F:27-34/Region: nucleotide-binding motif A (P-loop)

Query Match 52.6%; Score 729; DB 2; Length 276;
Best Local Similarity 56.4%; Pred. No. 2.1e-47;
Matches 146; Conservative 45; Mismatches 66; Indels 2; Gaps 2;

QY 16 TPLASALSVDLSLTIEDGSGTALIGHTSGKSTILQNLGLLVPSQSVRVFDLTITSTS 75
DB 3 TPFERLALYDINASTKEGYSYAVVIGHTSGKSTILQNLGLLVPSQSVRVFDLTITSTS 75

QY 76 KKKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFGPNQFVSEEDAVKTAREKALVIGID 135
DB 76 KKKDKLKKLVGVFPQFAENQIFETVLKDVAFGPNQFVSEEDAVKTAREKALVIGID 135

QY 136 ESLDRSPFELSGQMRRAVIAIGLAMEPAILVLDDEPTAGLDPLGRKELMTLPKLLHQSG 195
DB 136 ESLDRSPFELSGQMRRAVIAIGLAMEPAILVLDDEPTAGLDPLGRKELMTLPKLLHQSG 195

QY 196 -MTVLVTHLMDVVAEYANQVVMKGRLVKGGKPSDVDFQVFWMESEVQLGVPKITAFCK 254
DB 196 -MTVLVTHLMDVVAEYANQVVMKGRLVKGGKPSDVDFQVFWMESEVQLGVPKITAFCK 254

QY 255 RL-ADRGVSFKRLPIKIE 272
DB 255 RL-ADRGVSFKRLPIKIE 272

QY 243 HLEAALGVRFNEPMLTIED 261
DB 243 HLEAALGVRFNEPMLTIED 261

C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

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RESULT 5
AGI1775
ABC transporter (ATP-binding protein) homolog lin2749 [imported] - Listeria innocua (str
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AGI1775
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AGI1775
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <GLA>
A:Cross-references: UNIPROT:Q8Y455; GB:AL592022; PIDN:CAC97975.1; PID:g16415285; GSPDB:G
A:Experimental source: strain Clip1262
C:Genetics:
A:Gene: lin2749
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
```

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Query Match 50.2%; Score 696.5; DB 2; Length 288;
Best Local Similarity 50.6%; Pred. No. 6.2e-45;
Matches 137; Conservative 54; Mismatches 73; Indels 7; Gaps 2;

QY 1 MGTALENVFTYQEGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTILQNLGLLVP 60
DB 1 MEIKLEQLGQCYQKNSPFKRALDNNVDFSGSYSAIIGHTGSGKSTILQNLGLLMT 60

QY 61 QGSVRVFDLTITSTSKNDIQRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 EKGITVGDEIRVAGVKQKLDRLKRVGVFQPEAQLFEETVEKDICFGPMNFGVSEED 120

QY 121 AVKTAKEKALVGDIDSLFDRSPFELSGGQMRVAIAGILAMEPAILLVLDDEPTAGLDPLG 180
DB 121 AKLRKKVIYEVGLTEBILSRSPFELSGGQMRVAIAGVLAAMDPEVLVLDDEPTAGLDPHG 180

QY 181 RKELMTLTKLH-QSGMTIVLVTHLMDVAEYANOVYVMEKRLVKGKPSDVFDQVWFM 239
DB 181 REIMEMFYNLHKEGLTTLVTHSMEDAARYAEKIVLMKAGTVLQIGTPREIFAQPDDEL 240

QY 240 EEVQLGVPKITAFCKRLADRGVSFKRLPIKI 270
DB 241 VDGLSLVPDVRP-----QGLFERKFNVLK 265
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RESULT 6
AH1399
ABC transporter (ATP-binding protein) homolog lmo2600 [imported] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH1399
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1399
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <GLA>
A:Cross-references: UNIPROT:Q8Y455; GB:NC_003210; PIDN:CAD00678.1; PID:g16412088; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2600
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Query Match 49.9%; Score 692.5; DB 2; Length 288;
Best Local Similarity 50.2%; Pred. No. 1.2e-44;
Matches 136; Conservative 55; Mismatches 73; Indels 7; Gaps 2;

QY 1 MGTALENVFTYQEGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTILQNLGLLVP 60
DB 1 MEIKLEQLGQCYQKNSPFKRALDNNVDFSGSYSAIIGHTGSGKSTILQNLGLLMT 60

QY 61 QGSVRVFDLTITSTSKNDIQRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 EKGITVGDEIRVAGVKQKLDRLKRVGVFQPEAQLFEETVEKDICFGPMNFGVSEED 120

QY 121 AVKTAKEKALVGDIDSLFDRSPFELSGGQMRVAIAGILAMEPAILLVLDDEPTAGLDPLG 180
DB 121 AKLRKKVIYEVGLTEBILSRSPFELSGGQMRVAIAGVLAAMDPEVLVLDDEPTAGLDPHG 180

QY 181 RKELMTLTKLH-QSGMTIVLVTHLMDVAEYANOVYVMEKRLVKGKPSDVFDQVWFM 239
DB 181 REIMEMFYNLHKEGLTTLVTHSMEDAARYAEKIVLMKAGTVLQIGTPREIFAQPDDEL 240

QY 240 EEVQLGVPKITAFCKRLADRGVSFKRLPIKI 270
DB 241 VDGLSLVPDVRP-----QGLFERKFNVLK 265
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RESULT 7
F97281
ABC-type transporter, ATPase component (cobalt transporters subfamily) CAC3101 [imported]
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: F97281
R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: F97281
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <KUR>
A:Cross-references: UNIPROT:Q97EK9; GB:AE001437; PIDN:AAK81041.1; PID:g15026166; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3101
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Query Match 49.2%; Score 683; DB 2; Length 286;
Best Local Similarity 47.7%; Pred. No. 6.3e-44;
Matches 133; Conservative 62; Mismatches 80; Indels 4; Gaps 3;

QY 1 MGTALENVFTYQEGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTILQNLGLLVP 60
DB 1 MPKIENLTYYTYPGTFPEKALDNNITIEDGEFAVFIGTSGKSTILQNLGLLKPT 60

QY 61 QGSVRVFDLTITSTSKNDIQRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 SGIPIFDD--VDITDSKVLNDRKRVGLVFOYQPEVQLFEETIEKIDIAFGPRNGLSEEE 118

QY 121 AVKTAKEKALVGDIDSLF--DRSPFELSGGQMRVAIAGILAMEPAILLVLDDEPTAGLDPL 179
DB 119 VSTRVKKAMKMWGLEYNDFKDKSPFELSGGQMRVAIAGVVAEMPKVLIIDDEPTAGLDPK 178

QY 180 GRKELMTLTKLHQS-GMTIVLVTHLMDVAEYANOVYVMEKRLVKGKPSDVFDQVWF 238
DB 179 GRDDILYEIKKLQKEYNTIILVSHMEDVAKVADKIFVWYDSRCILSGNLDELVEFNEDT 238

QY 239 MEESVGLGVPKITAFCKRLADRGVSFKRLPIKIEFKESL 277
DB 239 LEKVLAVPKVTYLVKRLREKGFDSKDITIEAAKKEI 277

RESULT 8
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E83670
ABC transporter (ATP-binding protein) BH0165 [imported] - Bacillus halodurans (strain C-
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
C:Accession: E83670
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4333, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: E83670
A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <STO>
A:Cross-references: UNIPROT:Q9KGD6; GB:BA000004; NID:g10172612; PIDN:BA8038
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0165
C:Superfamily: ATP-binding cassette homology

Query Match 46.0%; Score 637.5; DB 2; Length 282;
Best Local Similarity 52.6%; Pred. No. 1.6e-40;
Matches 130; Conservative 44; Mismatches 72; Indels 1; Gaps 1;

QY 14 EGTPLAASLDSVSTIEDGSGKSTILQLLGLLVPSQSGSVRVPDLTITS 73
DB 2 KGSPEKVALSDVSTIPSGSFTAIIGTSGKSTLAQHFNGLLRPSKGTVRIGLELITA 61

QY 74 TSKNKDIRQKQGLVQFAENQIFFEETVLKDVAFQPNFQGVSEDAVKAREKALVG 133
DB 62 DQKPSLKEIRKVGVLQYPEHQLPFEETVEKDICFGPNYGVSEARAKRKLHLVG 121

QY 134 IDESLFDRSPFELSGQGMRRVAIAGILAMEPAAILVLDEPTAGLDPLGRKELMTLPKKLHQ 193
DB 122 LPDYLQASPLFSLSGQGMRRVAIAGILAMEPDVLVLDEPTAGLDPEGORLIMDMFYRLHQ 181

QY 194 -SGMTIVLVTHLMDVAEYANQVYMEKRLVKGKPSDVFODVVFMEEVGLVGPKITAF 252
DB 182 EKELTVLVTHNMSDAKPADQIIIVMSQGNVAMTGDRTQVFARADELVAGLDVVPETLQL 241

QY 253 CKRLADR 259
DB 242 LQVKER 248

RESULT 9
C90560
ABC transporter atp-binding protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004
C:Accession: C90560
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: C90560
A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <KUR>
A:Cross-references: UNIPROT:Q98QH4; GB:AL445566; PID:g14089801; PIDN:CAC13560.1; GSPDB:G
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU_3870
A:Genetic code: SGC3
C:Superfamily: ATP-binding cassette homology

Query Match 42.9%; Score 595.5; DB 2; Length 304;
Best Local Similarity 41.4%; Pred. No. 2.5e-37;
Matches 122; Conservative 66; Mismatches 88; Indels 19; Gaps 5;

QY 1 MGIALENVNTFYQEGTPLAASLSDVSLTIEDGSGKSTILQLLGLLVPS 60
DB 1 MQIIVKNISYIYNRKLTALKALDSSCIINGQEHVAIIIGTSGKTTFIEHNLALPIE 60
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61 QGSVR-VF-----DTLITST--SKNKDIRQKQGLVQFAENQIFFEETVL 104
DB 61 TGTINWIFENSHKTKKYLEVDVVLKRTYFKVKVCAKDIRRIGVVFQFAEQIFFEETIE 120

105 KDVAFGPNFQGVSEDAVKAREKALVGVDESIFDRSPFELSGQGMRRVAIAGILAMEP 164
DB 121 KDINFGPRSYGVSEAKQRAKYLEWVGLPLEPLEKNPFGLSGQGMRRVAIAGILALEP 180

165 AILVLDEPTAGLDPLGRKELMTLPKKLHQSGMTIVLVTHLMDVAEYANQVYMEKRLV 224
DB 181 DPLVLDEPTAGLDPLGRKELMTLPKKLHQSGMTIVLVTHLMDVAEYANQVYMEKRLV 240

225 KGGKPSDVFODVVFMEEVGLVGPKITAFCKELADRGVSFKELPI-KIEEFKESLN 278
DB 241 RDAQTYEILKDEKFLVENKSLPKLITFVNKLEORGIFLK--PVTSIDKLAIELN 293

RESULT 10
H90018
hypochemical protein SA2020 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2004
C:Accession: H90018
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci
ma, A.; Mizutani-Ti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90018
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <KUR>
A:Cross-references: UNIPROT:Q99S48; GB:BA000018; PID:g13702021; PIDN:BA843313.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2020
C:Superfamily: ATP-binding cassette homology

Query Match 42.5%; Score 589.5; DB 2; Length 286;
Best Local Similarity 44.8%; Pred. No. 6.5e-37;
Matches 112; Conservative 61; Mismatches 76; Indels 1; Gaps 1;

QY 1 MGIALENVNTFYQEGTPLAASLSDVSLTIEDGSGKSTILQLLGLLVPS 60
DB 1 MTRIPDNVSYTYQKGTPTQHOAIHVNTEPESQGYAIVGQTGSGKSTLIQINALLKPT 60

61 QGSVRVPDLTITSTSKNKDIRQKQGLVQFAENQIFFEETVLKDVAFQPNFQGVSEED 120
DB 61 TGTVTVDITTHTKDKYIIPVRKRIGMVQFPFESQLFEDTVREMIFGPNFKNWILDE 120

121 AVKTAREKALVGVDESIFDRSPFELSGQGMRRVAIAGILAMEPAAILVLDEPTAGLDPLG 180
DB 121 AKNYAHRLLMDLGFSDRVMSQSPFGSGQGMRRVAIAGILAMEPAAILVLDEPTAGLDPLG 180

181 RKELMTLPKKLH-QSGMTIVLVTHLMDVAEYANQVYMEKRLVKGKPSDVFODVVFPM 239
DB 181 KRQVNRLLKSLQTDENKAIILISHDMNEVARYADEVIYMEKGSIVQSTSPKELPKDKKL 240

240 EEVVLGVGPKI 249
DB 241 ADWHIGLPEI 250

RESULT 11
I64219
membrane transport protein (glnQ) homolog MG180 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 16-Aug-2004
C:Accession: I64219
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.J.
, C.A.; Venter, J.C.
```

Science 270, 397-403, 1995
A>Title: The minimal gene complement of Mycoplasma genitalium.
A;Accession: A64200; MUID:96026346; PMID:7569993
A;Accession: I64219
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-304 <TIGR>
A;Cross-references: UNIPROT:P47426; GB:U39695; GB:L43967; NID:g1045864; PID:g1045864; TIGR:P47426
A;Genetic code: SGC3
A;Start codon: GTG
A;Superfamily: ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;37-236/Domain: ATP-binding cassette homology <ABC>
F;54-61/Region: nucleotide-binding motif A (P-loop)

Query Match 39.0%; Score 540.5; DB 2; Length 304;
Best Local Similarity 40.2%; Pred. No. 3.3e-33;
Matches 113; Conservative 55; Mismatches 108; Indels 5; Gaps 2;

QY 3 IALENNFTYQEGTPLASAAALSDVSTIEDGVTALIGHTSGKSTILQLLNGLLVPSSQ 62
DB 17 LAVSHLSVFNSTNNPIKVIDDFSYTFQGNQIYCIIGDSGSGKSTLVNHFNGLIKPNQ 76

QY 63 SVRVFTLLI-TSTSKNKDRIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEDA 121
DB 77 DIWVKDIYIGAKQKIKNFKLRKRTISIVFPFQYQLFKDVTVEKDMFGFVALGQSKYDA 136

QY 122 VKTAREKALVGDIESLFDSPSPFELSGGQRRVAIAGILAMEPAIILVDEPTAGLDPLGR 181
DB 137 RQAAAYLEMMGUKYFPLENPFELSGGQRRVAIAGILAEIPELIFDEPTAGLDPEGE 196

QY 182 KELMTLFFKLLHSGMTIVLVTHLMDVVAENQVYVMEKGRVKGKSPDVFODVVFME 241
DB 197 REMWQLIKTAQQQRTVFMITHQMNVLVADVVLVLAAGLVKVAASPYEVFMDQTFLEK 256

QY 242 VOLGVPKITAFCKRLADRGVSKRL-----PIKIEEPKESLN 278
DB 257 TTIVPPVIOVKDLIAINAHFNKLQELQKLEQLASAIN 297

RESULT 12
S62814
histidine transport ATP-binding protein hisP - Mycoplasma pneumoniae (strain ATCC 29342)
N;Alternate names: glutamine transport protein GlnQ homolog; hypothetical protein G9_04
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 16-Aug-2004
R;Hilbert, H.; Himmelfreid, R.; Plagens, H.; Herrmann, R.
Nucleic Acids Res. 24, 628-639, 1996
A;Title: Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: S62797; MUID:96177562; PMID:8604303
A;Accession: S62814
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-303 <HIL>
A;Cross-references: UNIPROT:Q50293; EMBL:U34795; NID:g1215683; PID:AAC43687.1; PID:g121
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Himmelfreid, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73963
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-303 <HIM>
A;Cross-references: EMBL:AE000061; GB:U00089; NID:g1674336; PID:AAB96285.1; PID:g167434
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Genetics:
A;Gene: hisP
A;Genetic code: SGC3

C;Superfamily: ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;37-236/Domain: ATP-binding cassette homology <ABC>
F;54-61/Region: nucleotide-binding motif A (P-loop)

Query Match 38.5%; Score 533.5; DB 2; Length 303;
Best Local Similarity 39.5%; Pred. No. 1.1e-32;
Matches 111; Conservative 58; Mismatches 107; Indels 5; Gaps 2;

QY 3 IALENNFTYQEGTPLASAAALSDVSTIEDGVTALIGHTSGKSTILQLLNGLLVPSSQ 62
DB 17 LSVNLSCEFFNEKTVHEVKVIDNFSTTFANKVYCIIGDSGSGKSTLVNHFNGLIKPAYG 76

QY 63 SVRVFTLLI-TSTSKNKDRIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEDA 121
DB 77 DIWVKDIYIGAKQKIKNFKLRKRTISIVFPFQYQLFKDVTVEKDMFGFVALGQSKNEA 136

QY 122 VKTAREKALVGDIESLFDSPSPFELSGGQRRVAIAGILAMEPAIILVDEPTAGLDPLGR 181
DB 137 RQAAAYLEMMGUKYFPLENPFELSGGQRRVAIAGILAEIPELIFDEPTAGLDPEGE 196

QY 182 KELMTLFFKLLHSGMTIVLVTHLMDVVAENQVYVMEKGRVKGKSPDVFODVVFME 241
DB 197 REMWQLIKTAQQQRTVFMITHQMNVLVADVVLVLAAGLVKVAASPYEVFMDQTFLEK 256

QY 242 VOLGVPKITAFCKRLADRGVSKRL-----PIKIEEPKESLN 278
DB 257 TTIVPPVIOVKDLIAINAHFNKLQELQKLEQLASAIN 297

RESULT 13
G64435
cobalt transport ATP-binding protein O homolog - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
A;Accession: G64435
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.;
rsen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: G64435
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-279 <BUL>
A;Cross-references: UNIPROT:Q58488; GB:U67551; GB:L77117; NID:g1591728; PIDN:AAB99089.1;
C;Genetics:
A;Map position: REV1027976-1027137
C;Superfamily: ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;37-215/Domain: ATP-binding cassette homology <ABC>
F;37-44/Region: nucleotide-binding motif A (P-loop)

Query Match 36.9%; Score 511.5; DB 2; Length 279;
Best Local Similarity 42.1%; Pred. No. 4.4e-31;
Matches 107; Conservative 53; Mismatches 73; Indels 21; Gaps 4;

QY 3 IALENNFTYQEGTPLASAAALSDVSTIEDGVTALIGHTSGKSTILQLLNGLLVPSSQ 62
DB 4 VETKDLVFRYPDGT-----AVLKGINFKVKGEMVSLGPNAGAGKSTLFLHFNGLIRPTKG 59

QY 63 SVRVFTLLI-TSTSKNKDRI-----QIRKQVGLVFOFAENQIFETVLKDVAFQPNFG 115
DB 60 EVLI-----KGKPIKYDKSLVEVRKTVGLVFNQPDQIFAPTVADVAPGPNLNG 110

QY 116 VSEDAVKTAAREKALVGDIESLFDSPSPFELSGGQRRVAIAGILAMEPAIILVDEPTAG 175
DB 111 LPKEEVEKRVKEALKAVGM-EGENKPPHLSGGQKRVAGIAGLANQPEVIVLDEPTAG 169

QY 176 LDPLGRKELMTLFFKLLHSGMTIVLVTHLMDVVAENQVYVMEKGRVKGKSPDVFOD 235

[illegible]

A:Accession: D83670
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-278 <STO>
A:CROSS-references: GB:A001507; GB:BA000004; NID:g10172612; PIDN:BA030893.1; C:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0164
A>Note: ybxA
C:Superfamily: ATP-binding cassette homology

	Query Match	34.9%	Score 484;	DB 2;	Length 278;
	Best Local Similarity	41.3%	Pred. No.	5.1e-29;	
	Matches 116;	Conservative	57;	Mismatches 90;	Indels 18; Gaps
Qy	2	GIALENNFTYOBGTPLASAAALSVSLTIEPGSYTALIGHTSGKSTLIQLLNLGLLVPSQ	61		
Db	4	GLLLESVSYQYDAN--AAPVLKEIDIHVPLGEWAVIIPNGSCKSTLAKLINGLLLPST	60		
Qy	62	GSRVVFDTLITSTSKNKDIRQIRKOVGLGVFAENQIFEEETVLKDVAFGPQNFGVSEEDA	121		
Db	61	GRV-TFNGM--STWDGTHWEIRQQVGILVFONPEHQFVATTVRDDLAFGMENRGFPREKM	117		
Qy	122	VKTAREKIALVIGIDESLFDSPFFELSSGGQMERRVAIAGILAMEPAFLVLDEPTAGLDPLGR	181		
Db	118	IQRTEEVSIOQGIDH-LLDDEPHRLSGQKQKQRAIAGILAVEPSVIVFEATSMLDPOQR	176		
Qy	182	KELMTLFKLLHQSGMTIVLTHLMDDVAEYANQVVMEKGRLVKGKESDVQDVVPHEE	241		
Db	177	KDLVELTKQLHENGMTIIISITHDYNE-ASQAGRVLLEKGEVMLDGSPA-----VVFHBQ	230		
Qy	242	VOL--GVPKITAFCRKA--DRGVSFKRLPIKIEEFKESL	277		
Db	231	DXLEAAGIDRFAPYLQQLAQSRGIQLEGALLKKELVEAL	271		

Search completed: October 28, 2005, 17:53:46
Job time : 42 secs

RESULT 15
T44412
ABC transporter (ATP-binding protein) BH0164 [imported] - *Bacillus halodurans* (strain C-
C/Species: *Bacillus halodurans*
C/Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 16-Aug-2004
C/Accession: T44412; D83670
R/Takami, H.; Takaki, Y.; Nakasone, K.; Hirama, C.; Inoue, A.; Horikoshi, K.
Biosci. Biotechnol. Biochem. 63, 452-455, 1999
A>Title: Sequence analysis of a 32-kb region including the major ribosomal protein gene
A/Reference number: Z22756; MUID:59209008; PMID:1012928
A/Accession: T44412
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residue type: *TAAC*
A/Cross-references: UNIPROT:Q929J3; EMBL:AB017508; NID:G4512395; PIDN:BAW75300.1; PID:94
A/Experimental source: strain C-125
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A/Reference number: AB3650; MUID:20512582; PMID:11058132